SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # :_____ Date: _____
Art Unit: _____ Phone Number 30_____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _P. Schreiber_	NA Sequence (#) _2_	STN _____
Searcher Phone #: _308-4292_	AA Sequence (#) _____	Dialog _____
Searcher Location: _CM1 12E18_	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _9/24_	Bibliographic _____	Dr.Link _____
Date Completed: _9/24_	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _5_	Fulltext _____	Sequence Systems _GCG FastPB Ig Fast PB_
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time: _20_	Other _____	Other (specify) _____

PTO-1590 (1-2000)

From:	Portner, Ginny
Sent:	Friday, September 21, 2001 11:16 AM
To:	STIC-Biotech/ChemLib
Subject:	FW: 09/252,691

actually , I don't need the sequence searched against the entire data base but only need SEQ ID NO 1394 searched against the following seqeunces. Thanks

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```
ID   PSI_RSU; PATTERN.
AC   PS01149;
DT   NOV-1995 (CREATED); JUL-1999 (DATA UPDATE); JUL-1999 (INFO UPDATE).
DE   Rsu family of pseudouridine synthase signature.
PA   G-R-L-D-x(2)-[STA]-x-G-[LIVFA]-[LIVMF](3)-[ST]-[DNST].
NR   /RELEASE=38,80000;
NR   /TOTAL=18(18); /POSITIVE=18(18); /UNKNOWN=0(0); /FALSE_POS=0(0);
NR   /FALSE_NEG=0; /PARTIAL=0;
CC   /TAXO-RANGE=???P?; /MAX-REPEAT=1;
DR   P35159, RLUB_BACSU, T; P33918, RSUA_ECOLI, T; P45124, RSUA_HAEIN, T;
DR   O51155, Y129_BORBU, T; Q55578, Y361_SYNY3, T; O66829, Y554_AQUAE, T;
DR   P72581, Y612_SYNY3, T; P42395, YCIL_BUCAP, T; P37765, YCIL_ECOLI, T;
DR   P45104, YCIL_HAEIN, T; P55986, YE59_HELPY, T; O67444, YE64_AQUAE, T;
DR   P32684, YJBC_ECOLI, T; P75966, YMFC_ECOLI, T; P44827, YMFC_HAEIN, T;
DR   O05668, YRSU_MYCLE, T; O33210, YRSU_MYCTU, T; O32068, YTZF_BACSU, T;
DO   PDOC00885;
```

Thanks

CRPE

Original Message-----

Fr m:	Portner, Ginny
//	
Sent:	Friday, September 21, 2001 11:05 AM
T :	STIC-Biotech/ChemLib
Subject:	09/252,691

Please search SEQ ID No 1394.

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

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> 0 <
OI IO  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-252-691c-1394.res made by sdavid on Mon 24 Sep 101 9:37:35-PDT.

Query sequence being compared:US-09-252-691C-1394 (1-669)
Number of sequences searched:                              7
Number of scores above cutoff:                             7

Results of the initial comparison of US-09-252-691C-1394 (1-669) with:
       File : portner691.seq
```

```
                                                                            Init. Opt.
Sequence Name    Description                             Length Score Score  Sig. Frame
-------------    -----------                             ------ ----- -----  ---- -----
                 **** 1 standard deviation above mean ****
 1. l09228       TOIG of: l09228  check: 8816   28206   88    318    1.63    0
 2. u00008       TOIG of: u00008  check: 8999   39149   77    291    1.16    0
                 **** 0 standard deviation from mean ****
 3. z99116       TOIG of: z99116  check: 4068   218470  52    288    0.09    0
 4. ae000213     TOIG of: ae000213  check: 187  10959   35    288   -0.65    0
 5. ae000308     TOIG of: ae000308  check: 691  11961   35    302   -0.65    0
 6. d90748       TOIG of: d90748  check: 3982   15007   34    292   -0.69    0
 7. d90749       TOIG of: d90749  check: 928    20284   31    289   -0.82    0
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```
1. US-09-252-691C-1394 (1-669)
   l09228       TOIG of: l09228  check: 8816  from: 1  to: 28206

TOIG of: l09228  check: 8816  from: 1  to: 28206

LOCUS       BACDIA      28206 bp    DNA            BCT      26-MAY-1995
DEFINITION  Bacillus subtilis spoVA to serA region.
ACCESSION   L09228
VERSION     L09228.1  GI:410114
KEYWORDS    3-dehydroquinate dehydratase; aroC gene; diaminopimelate
            decarboxylase; lysA gene; penicillin-binding protein;
            peptidyl-prolyl isomerase; phosphoglycerate dehydrogenase; ppiB
            gene; response regulator; response regulator kinase; ribA gene;
            ribB gene; ribD gene; ribG gene; ribH gene; ribT gene; riboflavin
            biosynthesis operon; serA gene; signal peptidase; sipS gene; spoA
            gene; spoVAF gene.
SOURCE      Bacillus subtilis (strain 168, sub_species Marburg) DNA.
  ORGANISM  Bacillus subtilis
            Bacteria; Firmicutes; Bacillus/Clostridium group;
            Bacillus/Staphylococcus group; Bacillus.
REFERENCE   1 (bases 1 to 28206)
  AUTHORS   Yamamoto,J., Shimizu,M. and Yamane,K.
  TITLE     Molecular cloning and analysis of nucleotide sequence of the
            Bacillus subtilis lysA gene region using B. subtilis phage vectors
            and a multi-copy plasmid, pUB110
  JOURNAL   Agric. Biol. Chem. 55 (6), 1615-1626 (1991)
  MEDLINE   91345841
REFERENCE   2 (bases 1 to 28206)
  AUTHORS   Buchanan,C.E. and Ling,M.L.
  TITLE     Isolation and sequence analysis of dacB, which encodes a
            sporulation-specific penicillin-binding protein in Bacillus
            subtilis
  JOURNAL   J. Bacteriol. 174 (6), 1717-1725 (1992)
  MEDLINE   92193254
REFERENCE   3 (bases 1 to 28206)
  AUTHORS   Sorokin,A., Zumstein,E., Azevedo,V., Ehrlich,S.D. and Serror,P.
  TITLE     The organization of the Bacillus subtilis 168 chromosome region
            between the spoVA and serA genetic loci, based on sequence data
  JOURNAL   Mol. Microbiol. 10 (2), 385-395 (1993)
  MEDLINE   95020538
FEATURES             Location/Qualifiers
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                     /strain="168"
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                     /db_xref="taxon:1423"
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                     RPDVAANHVLEGHVIIVDTSPSVIITPTLFHHVQHAEEYRQAPSVGTFLRWVRFFG
                     ILASTLFIPIWFLFVLQPDLLPDNMKFIGLNKDTHIPIILQIFILADLGIEFLRMAAIH
```

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                                          *
                          *  *
       | -- | -- | -- | -- | -- | -- | -- |  *  *  ||  *
SCORE  0  20  29  39  49  59  68  78  88  2
STDEV  10  -1      0   1   1   68
```

```
              PARAMETERS
Similarity matrix   Unitary
Mismatch penalty    1          K-tuple              4
Gap penalty         1.00       Joining penalty     30
Gap size penalty    0.33       Window size         32
Cutoff score        0
Randomization group 0

              SEARCH STATISTICS

Scores:        Mean      Median    Standard Deviation
               50        36        23.25

Times:         CPU                 Total Elapsed
               00:00:00.09         00:00:01.00

Number of residues:                344036
Number of sequences searched:      7
Number of scores above cutoff:     7

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
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                EAHTHDYITTGQEDSKFGPDLHNQCTERAIEQVLQSEHIQLLGVHCHIGSQIFDTAGF
                VLAAEKIFKKLDEWRDSYFVSKVLNLGGGFGIRYTEDDEPLHATEYVEKIIEAVKEN
                ASRYGFDIPEIWIEPGRSLYGDAGTTLYTVGSQKEVPGVRQYVAVDGGMNDNIRPALY
                QAKYEAAAANRIGEAHDKTVSIAGKCCESGDMLIWDIDLPEVKEGDLAVFCTGAYGY
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CDS             complement(2693. .3565)
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                THNISGITDEMYLNALMTAGVKDAKVYVTAPFEVSGTAALTGLIKAYEVSSDRAISED
                VKQVANQELVTTSELGDKIGNENAAALIAKIKEEFAKNGVPDNKADIEKQVDDAASDL
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                /db_xref="GI:410119"

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                FTKKQIAGTSKFVFYPFNEMRKTN"
terminator      7299. .7323
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-35_signal      7388. .7393
                /gene="sipS"
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terminator      7872. .7911
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gene         8266. .9351
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CDS          8266. .9351
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             LDTVLSIPEDAKVICDQIAPTWIFTTARADEKKKRLSAFGVNIFLETERIQIPDVL
             KILAEEGIMSVYVEGGSAVHGSFVKEGCFQEIIFYFAPKLIGGTHAPSLISGEGFQSM
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             CEIMNEDGTMARVPELIEIAKKHQLKMITIKDLIQYRYNLTTLVEREVDITLPTDFGT
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CDS          13023. .13778
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CDS          14416. .14955
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conflict     15664. .15670
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terminator    17348..17360
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-10_signal    17418..17421
              /note="putative; ORFX13"

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misc_signal   18150..18170
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misc_signal   18185..18203
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-10_signal    18224..18229
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CDS           18803..20431
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CDS           20567..21625
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misc_signal   21645..21660
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              /note="homology with E. coli Pho-box; putative"

misc_signal   complement(21671..21687)
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              /note="homology with E. coli Pho-box; putative"

CDS           21706..22428
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CDS           22425..24194
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terminator    24231..24263
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misc_signal   24291..24310
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              /note="homology with E. coli Fur-box; putative"

-35_signal    24340..24345
              /note="putative; ORFX20-ORFX21"

misc_signal   24340..24356
              /standard_name="iron box"
              /note="homology with E. coli Fur-box; putative"

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              /note="putative; ORFX20-ORFX21"

CDS           24398..24982
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       IPTFIDEVEIKEKPKQKELSIRVHQPATAFSIKDDTLLKKLLKESLKWSPYEKVKFLS
       DQNETGVRIGSYGFTEISIPKQSKRSYLYQNKQGQDFLVPSNHSFDTVKEAIKEME
       SSSOEDTTPLIQAGAVQSVTIKQKHLYMRFSKESEVDDSIAGILMIEGLLLTAKEFGF
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terminator   26019..26053
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gene   26073..26903
       /gene="aroC"

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       /gene="aroC"
       /note="putative"

-10_signal   26096..26101
       /gene="aroC"
       /note="putative"

protein_bind   26130..26139
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       /note="putative"
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CDS   26136..26903
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       /db_xref="GI:410145"
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       SAIQTKDIDLIDIELFSGDANVKALVSLAEENNYYVVMSNHDFEKTPVKDEIISRLRK
       MQDLGAHIPKMAVMPNDTGDLLTLLDATYTMKTIYADRPIITMSMAATGLISRLSGEV
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terminator   26909..26944
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gene   complement(26946..28206)
       /gene="serA"

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BASE COUNT   8529 a   5565 c   6530 g   7582 t
ORIGIN

L09228 Length: 28206 September 24, 2001 09:27 Type: N Check: 8816 ..

Initial Score   =   88   Optimized Score   =   318   Significance   =   1.63
Residue Identity =   52%   Matches   =   380   Mismatches   =   255
Gaps   =   Conservative Substitutions = 94   Gaps   =   0

```
                                 X             10            20
                    GCTATAATGCGGCAATTGA-TA
                    | ||| || | ||||| |||  ||
CATGGAAAGACTGCAAAAAGTGATTGCTCATCCGGAGTTGCGTCGGCAGCAAGGCAGAAG-AGCTGATTA
17440     17450      17460      17470      17480      17490      17500
```

```
                       30            40            50            60            70            80
ACGGCTGAAAA-TA-CCAATGA--CGAAAACTTCTTTTAGAAAACACCGGTTGAG-----CGATTCAGCTCA
| |||      ||  |||||    |  ||||||| ||||||||||| ||||||||      ||| |||| | ||
AGAAGGAAAAGTAAAGGTCAATGCAAAGT--AGTAACAGAGCTAGGTGTTAAGGTCACCGGTTCTGATCA
17510      17520      17530      17540      17550      17560      17570
```

```
          90            100           110           120           130           140           150
CGA--CAAGCCACCAGAAGACGCCAGAACCCCAACGCGGGT---CATACTGTTCAATAAACCCTACG
|      ||| ||||||| | || |||  ||| || |  |||      ||| |||||||| | || |||
-GATTGAGGTAAACGGTTAAAGGTTGAACGCGA---AGAGCCGGTTACTTCTTCTCTTATATAAACC--AAG
17580      17590      17600      17610      17620      17630      17640
```

```
          160           170           180           190           200           210
ATG---TATTGCCCAGTTTACCGACGAGGCCGGCGCACGCTGAAGGAC-TTTATCCCCGTA------C
         ||| |||||  |  | | |||| |||||| | |  |||||||  ||||    | |       |
AGGGCTTATTTCCGCAGCGCA-AGATGATAAAGGACGCAAAGTGGTGACCGGACTTTTTTAAAAATATTCCGC
17650      17660      17670      17680      17690      17700      17710
```

```
          220           230           240           250           260           270           280
AGGGAGTCTACGCAGCGGGACGTCTGGATCGCGAAGCTGGAG-GGCTGCTGGTCCTTACCAACGACGGGC--
|| |  |  |||  | | |||  | || | ||    | ||||    ||| | || ||| | ||| ||| |||
AGCGGCATTTATCCGATTGGGCGTCTGGACTATGATA-CGAGCCGGTGTCTTTTGCTTTAACCAATGACGGGCGAA
17720      17730      17740      17750      17760      17770      17780
```

```
          290           300           310           320           330           340           350
TGCTTCCAGGCCAGGCTTACTCACCGGGCAAACGTACCGGAAAAATTTACTATGTGCAGGTTGAAGGCGAGC
|  |||  | | | |||     |  |   ||| | | | ||  |     || |   |||| | |||| | |||
TTCGCCA--ATAAGCTAATGCATCCTAAGTATGAAATAGACAAAACATACGTGGCGAAGGTGAAAGGAATCC
17790      17800      17810      17820      17830      17840      17850
```

```
          360           370           380           390           400           410           420
CGGACGACGCGTCGCTGGCAAAGCTGCGCAACGGCGTAACGCTGGCGACGACGTCCCACCCTGCCGGCCTGGTA
||    |    | |  | ||| ||||| | ||| | | | |  || ||| ||||  |   | || || || ||||
CGCCTAAAGAGCTGCTCAGAAAGCTGGAGGATTAGGCTGGAGGAAGG--CAAAACAG-CGCCTGCTA
17860      17870      17880      17890      17900      17910      17920
```

```
          430           440           450           460           470           480           490
TTGAACGTGTGAATGAACCCG--AGTGGCTGTGGCCGCGCA-ACCCGCCGATTCGTCGAGC-GTAAATCCAT-
|  | | |  | |  |||||    || |  | || | | | |   || |   || || ||||   ||||||  |
--AA--GCGAA-GCTGCTGTTCTTTGGATAAGAAGAAAAAGCAGACAAGC--ATTATTCAGCTGACGATCCATG
17930      17940      17950      17960      17970      17980
```

```
          500           510           520           530           540           550
TCCTAC-CAGCTGGTTAAATCACC-CTT-TATGAAGGCCGCAACCGAC---AGTT--CAGGCGCATGAC
| ||    ||| || |||| |||      || |||||| || | ||||      ||    | || |  |||
AGGGACGCAACAGAC--AAGTGCGCCGCCATGTTTGAAG--CG-ATCGGACATGAGGTAATCAAGCTGAAGCCG
17990      18000      18010      18020      18030      18040      18050
```

```
          560           570           580           590           600           610           620
TGCCCATGTGGGCTTCCCTACCCTGCGACTCATTCGCTAC--GCCATGGCAGCTA--TACGCTGGACTCGC
||| ||| || || |  || ||  | ||  | | | | |     |||| ||||| ||    ||| | | ||| ||
TGAGGAATACGCGTTTTAAACCTGCGGCCTGCAC-ACGGCGAT-GCCAGAGTTACGC--CTCACGA
18060      18070      18080      18090      18100      18110      18120
```

```
          630           640           650           660                   X
TGGCAAACGG------GGAATGGCGG--GATGTT----ACCC---CTAAGGAGAACTGA
|| |   | |       |||| |||      |||| | |      |   |   ||||||||
AGTAAAAAGGCTCAGAGAATGAACGTCCAGATCACGGTAAAAACGCTTTCTAAATTTCACATAACCTTCAAAAAGT
18130      18140      18150      18160      18170      18180      18190
```

```
AAGAAATGTGAAATGAACGTCCAATGATATAATTGAA
18200      18210      18220      18230
```

2. US-09-252-691C-1394
    u00008   TOIG of: u00008   check: 8999   from: 1   to: 39149

TOIG of: u00008   check: 8999   from: 1   to: 39149

LOCUS   ECOHU49   39149 bp   DNA   BCT   10-FEB-1994
DEFINITION   centisome 49 region of E.coli K12 BHB2600.
ACCESSION   U00008
VERSION   U00008.1   GI:453985

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KEYWORDS    .
SOURCE      Escherichia coli K12 BHB2600.
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1  (bases 1 to 39149)
  AUTHORS   Richterich,P., Lakey,N., Gryan,G., Jaehn,L., Mintz,L., Robison,K.
            and Church,G.M.
  TITLE     Automated multiplex sequencing of the E.coli genome
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 39149)
  AUTHORS   Robison,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-SEP-1993) Department of Genetics, Harvard Medical
            School, 200 Longwood Avenue, Boston MA 02115
REFERENCE   3  (bases 1 to 39149)
  AUTHORS   Robison,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-1994) Department of Genetics, Harvard Medical
            School, 200 Longwood Avenue, Boston MA 02115
COMMENT     On Feb 10, 1994 this sequence version replaced gi:405903.
            From E.coli K12 BHB2600.  All of the sequence in this contig was
            sequenced at least twice on one strand and once on the other
            strand, except in the 2 regions marked.  The annotation of this
            sequence should be considered preliminary and incomplete.  Please
            contact KRobison@nucleus.harvard.edu before citing this sequence
            in a published work.
FEATURES             Location/Qualifiers
     source          1..39149
                     /organism="Escherichia coli"
                     /db_xref="taxon:562"
     gene            <1..4942
     CDS             <1..1230
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                     Homologous to ABC-type transporters; closest similarity to
                     oliopeptide transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
                     /note="weak match to heme-binding protein from
                     H.influenzae"
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                     TEYAARNYPDAAELVLLAPMKDLPSEVFTQIYQPPVSKGDGYDRDNLLKADKLLNEA
                     GGVLKGQQRVNATTAQGTGPLSFELLPASSNSQWVLPFQHSLQRLGINMDIRKVDNSQIT
                     NRMSRDYFDMPRWRAMPWPSSDLQISWSSEYINSTYNAPGVQSPVIDSLINQIIAA
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     CDS             1231..1620
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                     Homologous to ABC-type transporters; closest similarity to
                     oliopeptide transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
                     /note="probable integral membrane component of transport
                     complex (oligopeptides?); C-terminus may be truncated to
                     form yeJC"
                     /codon_start=1
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                     GNAGVLPGAGGEGVRASHAQTGVGNISDSNYRGGRGLDPEVIAEITHRYGFDKPIHER
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     CDS             /gene="probable transport operon; yeJA-yeJB/C-yeJE-yeJF.
                     Homologous to ABC-type transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
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                     complex"
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                     VGVVRAEFLRTRNFDYIRAAQALGVSDRSIILRHMLPNAMVATLFLPFILCSSITTL
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                     3353..4942
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                     Homologous to ABC-type transporters; closest similarity to
                     oliopeptide transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
                     /note="ABC-type ATP-dependent transport protein, perhaps
                     of oligopeptides"
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                     IVRKLAHRVAVMQNGRCVEQNYAATLFASPTHPYTQKLLNSEPSGDPVPLPEPASTLL
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                     complement(5623..6756)
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                     /db_xref="GI:424052"
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                     MVISALLGLGFWSLVGVAAFVGCVSMVSSNAMAVILDEFPHMAGTASSLAGTFRFGI
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                    from Buchnera aphidicola and orf near centisome 89"
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                    HDVAYDGNPLAQQHGPRYFMLNKPQGYVCSTDDPHPTVLYFLDEPVAWKLHAAGRLD
                    IDTTGLVLMTDDGQWSHRITSPRHCEKTYLVFTLESPVADDTAEQFAKGVQLHNEKDL
                    TKPAVLEVITPTQVRFITISEGRYHQVKRMFAAVGNHVVELHRERIGGITLDADLAPGE
                    YRPLTEEEIASVV"
CDS                 7156. .7659
                    /note="probably not expressed; yejD on opposite strand has
                    better dicodon usage"
                    /codon_start=1
                    /transl_table=11
                    /product="bicB/yejD"
                    /protein_id="AAA16407.1"
                    /db_xref="GI:405943"
                    /translation="MAARRSNAVRPLTIISHQHQTGGINIQPPRRMQFPRYRFIKKIE
                    HRWVIRVVRGANIALRLIEHEVTWTVLLRQRVAIVSDIMFRKQFERCITDDFAIDGDT
                    IAADFTPGNSTANAELLCDKFIKSHVCDFACKNGGRALTRKSELLSAQYSGLITSLKG
                    KRSMAYY"
CDS                 7685. .8896
                    /note="some similarity to a phage protein and
                    restriction-modification systems"
                    /codon_start=1
                    /transl_table=11
                    /product="yejH"
                    /protein_id="AAA16381.1"
                    /db_xref="GI:405911"
                    /translation="MIFTLRPYQQEAVDATLNHFRRHKTPAVIVLPTGAGKSLVIAEL
                    ARLARGRVLVIAHVKELVAQNHAKYQALGLEADIFAAGLKRKESHGKVVFGSVQSVAR
                    NLDAFQGEFSLLIVDECHRIGDDEESQYQQILTHLTKVNPHLRLLGLTATPFRLGKGW
                    IYQFHYGHGMVRGDEKALFRDCIYELPLRYMIKHGYLTPPERLDMPVVQYDFSRLQAQS
                    NGLFSEADLNRELKKQQRITPHIISQIMEFAATRKGVMIFAATVEHAKEIVGLLPAED
                    AALITGDTPGAERDVLIENFKAQRFRYLVNVAVLTTGFDAPHVDLIAILRPTESVSLY
                    QOIVGRGLRLAPGKTDCLILDYAGNPHDLYAPEVGTPKGSDNVPVQVFCPACGFANT
                    FWGKQRPPTGH"
gene                8812. .9162
                    /gene="yeiI -- may be frameshift fragment"
gene                9117. .9446
                    /gene="yejJ -- may be frameshift fragment"
CDS                 9571. .9861
                    /note="ribosomal protein L25"
                    /codon_start=1
                    /transl_table=11
                    /product="rplY"
                    /protein_id="AAA16413.1"
                    /db_xref="GI:405949"
                    /translation="MFTINAEVRKEQGKGASRRLRAANKFPAIIYGGKEAPLAIELDH
                    DKVMNMQAKAEFYSEVLTIVVDGKEIKVKAQDVQRHPYKPKCSTSTSFALNC"
repeat_region       9949. .9985
                    /rpt_family="REP/PU"
CDS                 complement(9993. .11000)
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                    /transl_table=11
                    /product="yejK"
                    /protein_id="AAA16382.1"
                    /db_xref="GI:405914"
                    /translation="MSLDINQIALHQLIRKDEQNLELVLRDSLLEPTETVVEMVAELH
                    RVYSAKNKAYGLFSESELAQTLRLQRQGEDFLAFSRAATGRLDELAKYPFADGGF
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                    PESTRYLTFLKGRVGRKVADFFMDFLGASEGLNAKAQNRGLLQAVDDFTAEAQLDKAE
                    RQNVRQQVYSCNEOLQAGEEIELKSLSKELAGVSEVSFTEFAAEKGYELEESFPADR
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CDS                 11182. .11409
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                    /product="yejL"
                    /protein_id="AAA16383.1"
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CDS                 /db_xref="GI:405915"
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                    INTSIAPAQRQAIANSFARALQSSINEDKAH"
                    11429. .13189
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                    TTLAGRIYSYVSIGHFSFLVFATYLILLFPLTFIVSGQRLMRFLSVILATAGMTLLL
                    IDSEVFTRFHLHNIPIVWQLVINPDENEMARDWQLMFISVPVILLELVFATWSWQKL
                    RSLTRRRFARPLAAFLFIAFIASHVVYIWADANFYRPITMQRANLPLSYPMTARRFL
                    EKHGLLDAQEYQRRLIEQGNPDAVSVQYPLSELRYRDMGTGQNVLLITVDGLNVSRFE
                    KQMPALAGFAEONISFTRHMSSGNTTDNGIFGLFYGISPSYMDGILSTRTPAALITAL
                    NQGGYQLGLFSSDGFTSPLYRQALLSDFSMPSVRTQSDEQTATQWINWLGRAYQEDNR
                    WFSWVSFNGTNIDDSNQQAFARKYSRAAGNVDDQINRVLNALRDSGKLDNTVVIITAG
                    RGIPLSEEETFDWSHGHLQVPLVIHWPGTPAQRINALTDHTDLMTTLMQRLLHVSTP
                    ASEYSQGQDLFNPQRRHYWVTAADNDTLAITTPKKTLVLNNNGKYRTYNLRGERVKDE
                    KPQLSLLLQVLTDEKRFIAN"
tRNA                13264. .13346
                    /gene="proL"
                    /note="codon recognized: CCC"
                    /product="tRNA-Pro"
gene                13264. .13346
                    /gene="proL"
                    /product="proL"
CDS                 complement(13443. .16010)
                    /partial
                    /note="strong match to pertactin from Bordetella.  No
                    start codonmay be missing some of N-terminus"
                    /codon_start=1
                    /transl_table=11
                    /product="yejO"
                    /protein_id="AAA16385.1"
                    /db_xref="GI:405918"
                    /translation="VSREEFPRLFAPSLYSPIALASTVEYGETVDGVVLEKDIQLVYG
                    TANTTKINPGGEQHIKEFGVSNNTEINGGYQYIEMNGAAEYSVLNDGYQIVQMGGAAN
                    QTTLNNGVLQVYGAANDTTIKGGRLIVEKDGGAVFVAIEKGGLLEVKEGGFAFAVDQK
                    AGGAIKTTRAMEVFGTNRLGQPDIKNGIANNMLLENGGSLRVEENDFAYNTTVDSGG
                    LLEVMDGGTVTGVDKKAGGKLIVSTNALEVSGPNSKGQFSIKDGVSKNYELDDGSGLI
                    VMEDTQRAIDTILDKHATMQSLGKDTGTKVQANAVYDLGRSYQNGSITYSSKAISENMV
                    INNGRANVWAGTMVNVSVRGNDGILEVMKPQINYAPAMLVGKVVVSEGASFRTHGAVD
                    TSKADVSLENSVWTIIADITTTNQNTLLNLANLAMSDANVIMMDEPVTRSSVTASAEN
                    FTTLTTNTLSGNGNFYMRTDMANHQSDQLNVTGQATGDFKIFVTDTGASPAAGDSLTL
                    VTTGGGDAAFTLGNAGGVVDIGTYEYTLLDNGNHSWSLAENRAQITPSTTDVLNMAAA
                    QPLVFDAELDTVRERLGSVKGVSYDTAMWSSAINTRNNVTTDAGAGFEQTLTGLTLGI
                    DSRFSREESSTIRGLIFGYSHSDIGFDRGGKGNIDSYTLGAYAGWEHQNGAYDGVVK
                    VDRFANTIHGKMSNGATAFGDYNSNGAGAHVESGFRWVDGLWSVRPYLAFTGFTTDGQ
                    DYTLSNGMRADVGNTRILRAEACTAVSYHMDLQNGTTLEPWLKAAVRQEYADSNQVKV
                    NDDGKFNNDVAGTSGVYQAGIRSSFTPFLSGHLSVSYGNGAGVESPWNTQAGVVWTF"
repeat_unit         15970. .17170
                    /rpt_family="IS5"
CDS                 17523. .18200
                    /note="regulatory protein narP"
                    /codon_start=1
                    /transl_table=11
                    /product="narP"
                    /protein_id="AAA16411.1"
                    /db_xref="GI:405947"
                    /translation="MILIKPQETTMPEATPFQVMIVDDHPLMRRGVRQLLELDPGSEV
                    VAEAGDGASAIDLANRLDIDVILLDLNMKGMSGLDTLNALRRDCVTAQIIILTVSDAS
                    SDVFALIDAGADGYLLKDSDPEVLLEAIRAGAKGSKVFSERVNQYLREREMFGAEEDP
                    FSVLTERELDVLHELAQGLSNKQIASVLNISEQTVKVHIRNLLRKLNVSRSRVAATILF
                    LQDRGAQ"
repeat_region       18231. .18385
                    /rpt_family="REP/PU"
CDS                 complement(18411. .19463)
                    /note="probably part of aeg-46.5 operon; homolog of
                    Rhodobacter ccl2"
                    /codon_start=1
                    /transl_table=11
                    /product="yejP"
                    /protein_id="AAA16386.1"
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          /db_xref="GI:405919"
          /translation="MRFLLGVLMLMISGSALATIDVLQFKDEAQEQQFRQLTEELRCP
          KCQNNSIADSNSMIATDLRQKVYELMQEGKSKKEIVDYMVARYGNFVTYDPPLTPLTV
          LLWVLPVVAIGIGGHVIYARSRRRVRVVPEAFPEQSVPEGKRAGYVYLPGIVVALIV
          AGVSYYQTGNYQQVKIWQQATAQAPALLDRALDPKADPLNEEEMSRLALGMRTQLQKN
          PGDIEGWIMLGRVGMALGNASIATDAYATAYRLDPKNSDRAALGYAEALTRSSDPNDNR
          LGGELLRQLVRTDHSNIRVLSMYAFNAFEQQRFGEAVAAWEMMLKLLPANDTRRAVIE
          RSIAQAMQHLSPQESK"
     CDS  complement(19460..20017)
          /note="probable thioredoxin; may be part of aeg-46.5
          operon"
          /codon_start=1
          /transl_table=11
          /product="yejQ"
          /protein_id="AAA16387.1"
          /db_xref="GI:405920"
          /translation="MKRKVLLIPLIIFLAIAAALLWQLARNAEGDDPTNLESALIGKP
          VPKFRLESLDNPGQFYQADVIFQGKPVLLNVWATWCPTCRAEHQYLNQLSAQGIRVGK
          MNYKDDRQKAISWLKELGNPYALSLFDGDGMLGLDLGVVGAPETFLIDGNGIIRYRHA
          GDLNPRVWEEEIKPLWEKYSKEAAQ"
     CDS  complement(20014..21957)
          /note="may be part of aeg-46.5 operon; strong match to
          ccl from Rhodobacter and corresponding plastid proteins"
          /codon_start=1
          /transl_table=11
          /product="yejR"
          /protein_id="AAA16388.1"
          /db_xref="GI:405921"
          /translation="MMPEIGNGLLCLALGIALLLSVYPLWGVARGDARMMASSRLFAW
          LLFMSVAGAFLVLVNAFVVNDFTVTYVASNSNTQLPVWYRVAATWGAHEGSLLLWVLL
          MSGWTFAVAIFSQRIPLDIVARVLAIMGMVSVGFLLFLFTSNPFSRTLPNFPIEGRD
          LNPLLQDPGLIFHPLLLXMGYVGPSVAFAFAIASLLSGRLDSTYARFTRPWTLAAWIF
          LTLGIVLGSAWAYYELGWGGWWFWDPVENASFMPWLVGTALMHSLAVTEQRASPKAWT
          LLLAISAFSLCLLGTFLVRSGVLVSVHAFASDPARGMFILAFMVLVIGGSLLLFAARG
          HKVRSRVNNALWSRESLLLANNVLVAAMLVVLLGTLLPLVHKQLGLGSISIGEPFFN
          TMFTWLMVPFALLLGVGPLVRWGRDRPRKIRNLLIIAFISTLVLSLLLPWLFESKVVA
          MTVLGLAMACWIAVLAIAEAALRISRGTKTTFSYWGMVAAHLGLAVTTVGIAFSQNYS
          VERDVRMKSGDSVDIHEYRFTFRDVKEVTGPNWRGGVATIGVTRDGKPETVLVAEKRY
          YNTAGSMWTEAAIDGGIIRDLYAALGEELENGAWAVRLYYKPFVRWIWAGGLMMALGG
          LLCLFDPRYRKRRVSPQKTAPEAV"
     CDS  complement(21954..22433)
          /note="may be part of aeg-46.5 operon"
          /codon_start=1
          /transl_table=11
          /product="yejS"
          /protein_id="AAA16389.1"
          /db_xref="GI:405922"
          /translation="MNIRRKNRLWIACAVLAGLALTIGLVLVIALRSNIDLFYTPGEIL
          YGKRETQQMPEVGQLRVGGMVMPGSVQRDPNSLKVIFTIYDAEGSVDVSYEGILPDL
          FREGQGVVVQGELEKGNHILAKEVLAKHDENYTPPEVKAMEANHRRPASVKDPAS"
     CDS  complement(22430..22639)
          /codon_start=1
          /transl_table=11
          /product="yoJM"
          /protein_id="AAA16390.1"
          /db_xref="GI:453988"
          /translation="MTPAFASWNEFFAMGGYAFFWLAVVMTVIPLVVLVHSVMQHR
          AILRGVAQQRAREARLRAAQQQEAA"
    gene  complement(22636..22977)
          /gene="yejT -- may be frameshift fragment"
     CDS  complement(22881..23372)
          /note="homolog of helC from Rhodobacter; probably part of
          aeg-46.5 operon"
          /codon_start=1
          /transl_table=11
          /product="yejU"
          /protein_id="AAA16391.1"
          /db_xref="GI:405924"
          /translation="MWKTLHQLAIPPRLYQICGWFIPWLAIASVVVLTVGWIWGFGFA
          PADYQQGNSYRIIYLHVPAAIWSMGIYASMAVAAFIGLVWQMKMANLAVAAMAPIGAV
          FTFIALVTGSAWGKPMWGTWWVWDARLTSELVLLFLYVGVIALWHAFDDRRLAAVRQV
          SWC"
     CDS  complement(23414..24076)
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          /note="may be part of aeg-46.5 operon; homolog of
          Rhodobacter helB and corresponding plastid proteins"
          /codon_start=1
          /transl_table=11
          /product="yejV"
          /protein_id="AAA16392.1"
          /db_xref="GI:405925"
          /translation="MMFWRIFRLELRVAFRHSAEIANPLWFFLIVITLFPLSIGPEPQ
          LLARIAPGIIWVAALLSSLLALERLFRDDLQDGSLEQLMLLPLPAVVLAKVMAHWM
          VTGLPLLILSPIVAMLGMDVYGWQVMALTLLLGTPTLGFLGFGAPGVALTVGLKRGVL
          LSILVLPLTIPLLIFATAAMDAASMHLPVDGYLAILGALLAGTATLSPFATAAALRIS
          IQ"
     CDS  complement(24073..24690)
          /note="ABC-type ATP-dependent transporter; may be part of
          aeg-46.5 operon"
          /codon_start=1
          /transl_table=11
          /product="yejW"
          /protein_id="AAA16393.1"
          /db_xref="GI:405926"
          /translation="MLEARELLCERDERTLFSGLSFTLNAGEWVQITGSNGAGKTTLL
          RLLTGLSRPDAGEVLWQGQPLHQVRDSYHQNLLWIGHQPGIKTRLTALENLHFYHRDG
          DTAQCLEALAQAGLAGFEDIPVNQLSAGQQRVALARLWLTRATLWILDEPFTAIDVN
          GVDRLTQRMAQHTEQGGIVILTTHQPLNVAESKIRRISLTQTRAA"
     CDS  complement(24709..25311)
          /note="may be part of aeg-46.5 operon; strong similarity
          to nirT from P.stutzeri"
          /codon_start=1
          /transl_table=11
          /product="yejX"
          /protein_id="AAA16394.1"
          /db_xref="GI:405927"
          /translation="MGNSDRKPGLIKRLWKWRTPSRLAGTLLLIGFVGGIVFWGGF
          NTGMEKANTEEFCISCHEMRNTVYQEYMDSVHYNNRSGVRATCPDCHVPHEFVPKMIR
          KLKASKELYGKIFGVIDTPQKFEAHRLTMAQNEWRRMKDNNSQECRNCHNFEXMDTTA
          QKSVAAKMHDQAVKDGQTCIDCHGIAHKLPDMREVEPGF"
     CDS  complement(25281..25790)
          /note="may be part of aeg-46.5 operon; match to
          periplasmic nitrate reductase B subunit (napB) from
          Alcaligenes eutrophus; weak match to Human guanylate
          cyclase"
          /codon_start=1
          /transl_table=11
          /product="yejY"
          /protein_id="AAA16395.1"
          /db_xref="GI:405928"
          /translation="MEFGSEIMKSHDLKKALCQWTAMALAVVSGAVWAANGVDFSQSP
          EVSGTQEGAIRMPKEQDRMPLNYVNQPPMIPHSVEGYQVTTNTNRCLQCHGVESYRTT
          GAPRISPTHFMDSDGKVGAEVAPRRYFCLQCQYRRPIPRQSWGIPLPHQKVTGNKRLL
          WEILTVSLV"
     CDS  complement(25766..26629)
          /note="may be part of aeg-46.5 operon; weak match to
          ferredoxins"
          /codon_start=1
          /transl_table=11
          /product="yejZ"
          /protein_id="AAA16396.1"
          /db_xref="GI:405929"
          /translation="MANRKRDAGREALEKKGWRSHRWLVLRRLCQFFVLGMFLSGPW
          FGYWILHGNYSSSLLFDTVPLTDPLMTLQSLASGHLPATVALTGAVIITVLAYLAGKR
          LFCSWVCPLNPITDLANWLRRRFDLNQSATIPRHIRYVLLVVILVGSALTGTLIWEWI
          NPVSLMGRSLVMGFGSGALLILALFLFDLLVEHGWCGHICPCVGALYGVLGSKGVITV
          AATDRQKCNRCMDCFHVCPEPHVLRAPVLDEQSPVQVTSRDCMTCGRCVDVCSEDVFT
          ITRWSSGAKS"
     CDS  complement(26616..27008)
          /note="possible ferredoxin; GTG start codon; may be part
          of aeg-46.5 operon"
          /codon_start=1
          /transl_table=11
          /product="yoJA"
          /protein_id="AAA16397.1"
          /db_xref="GI:405930"
          /translation="MRITRAPKCAQAVRWIVRLNRSTTRGWGWRYWWTRKTVSTFRGL
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CDS
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                    RCDVCYRECPKIDEAITLELERNTRTGKHARFLPTVHSDACTGCGKCEKVCVLEQPAI
                    KVLPLSLAKGELGHHYRFGWLEGNNGKS"
     complement(26839..27312)
     /note="may be part of aeg-46.5 operon; weak match to
     several proteins with redox functions"
     /codon_start=1
     /transl_table=11
     /product="yojB"
     /protein_id="AAA16398.1"
     /db_xref="GI:405931"
     /translation="MSRSAKPQNGRRRPFLRDVVRTAGGLAAVGVALGLQQQTARASGV
                    RLRPPGAINENAFASACVRCGCQCVQACPYDFLKLATLASGLSAGTPYFVARDIPCEMC
                    EDIPCAKVCPSGALDREIESIDDARMGLAVLVDQENCLNFQGPALRCLLSRMPEN"
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CDS
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     complement(27319..29748)
     /note="may be part of aeg-46.5 operon; strong match to the
     periplasmic nitrate reductase large subunit (napA) from
     Alcaligenes eutrophus; GTG start codon"
     /codon_start=1
     /transl_table=11
     /product="yojC"
     /protein_id="AAA16399.1"
     /db_xref="GI:453989"
     /translation="MPVSACRAVARAVVGQQEAIKWDKAPCRFCGTGCGVLVGTQOGR
                    VVACQGPDAPVNRGLNCIKGYFLPIMYGKDRLRQPLLRMKNGKYDKEGEFTPITWD
                    QAFDVMEEKFKTALKEKGPESIGWIFGGSGWTWEGYAASKLFKAGFRSNNIDPNARHC
                    MASAVVGFMRTGCMDEPMGCYDDIEQADAFVLWGANMAEHMPILWSRITNRRLSNQNV
                    TVAVLSTYQHRSFELADNGIIFTPQSDLVILNYIANYIIQNNAINQDFFSKHVNLRKG
                    ATDIGYGLRPTHPLEKAKAKNPGSDASEPMSFEDYKAFVAEYTLEKTAEMTGVPKDQLE
                    QLAQLYADPNKKVISVTWMGFNQHTRGVWANNLVYNLHLLTGKISOPGCGPFSLTGQP
                    SACGTAREVGTFAHRLPADMVTNEKHRDICEKKWNIPSGTIPAKIGLHAVAQDRALK
                    DGKLNVYWTMCTNNMQAGPNINEERMPGWRDPRNFIIVSDPYPTVSALAADLILPTAM
                    WVEKEGAYGNAERRTQFWROQVQAPGEAKSDLWQLVQFSRRFKTEEVWPEDLLAKKPE
                    LRGKTLYEVLYATPEVSKFPVSELAEDQLNDESRELGFYLQKGLFEYAWFGRGHGHD
                    LAPFDDYHKARGLRWPVVNGKETQWRYSEGNDPYVKAGEGYKFYGKPDGKAVIFALPF
                    EPAAEAPDEEYDLWLSTGRVLEHWHTGSMTRRVPELHRAFPEAVLFIHPLDAKARDLR
                    RGDKVKAVKLEKV"
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misc_feature
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     29705..29959
     /note="CAUTION! Low coverage in this region of the
     sequence"
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CDS
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     /transl_table=11
     /product="yojF"
     /protein_id="AAA16400.1"
     /db_xref="GI:405935"
     /translation="MHTNWQVCSLVVQAKSERISDISTQLNAFPGCEVAVSDAPSGQL
                    IVVVEARDSETLIQTIESVRNVEGVLAVSLVYHQQEQGEETP"
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CDS
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     complement(30054..30548)
     /note="probable ferredoxin or Fe-S protein; probably part
     of aeg-46.5 operon"
     /codon_start=1
     /transl_table=11
     /product="yojG"
     /protein_id="AAA16401.1"
     /db_xref="GI:453990"
     /translation="MKIDASRRGILTGRWRASNGIRPPWSGDESHFLTHCTRCDACI
                    NACENNLQRGAGGYPSVNFKNNECSFCYACAQOACPESLFSPRHTRAWDLQFTIGDAC
                    LAXQSVECRRCQDSCEPMAIIFRPTLSGIYQPQLNSQLCNGCGACAASCPVSAITAEY
                    LHAH"
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CDS
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     30935..31144
     /note="DNA repair protein"
     /codon_start=1
     /transl_table=11
     /product="ecotin (protease inhibitor)"
     /protein_id="AAA16410.1"
     /db_xref="GI:453992"
     /translation="MKKESKKMKTILPAVLFAAFATTSAWAAESVQPLEKIAPYPQAE
                    KGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGIDYYVFD
                    KVSSPVSTMMACPDGKKEKKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKIRVWKAE
                    EKIDNAVVR"
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repeat_region
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     31533..31654
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repeat_region
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     31689..31711
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repeat_region
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     31814..31845
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repeat_region
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     31875..31981
     /rpt_family="REP/PU"
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repeat_region
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     31973..32018
     /rpt_family="REP/PU"
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repeat_region
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     32030..32096
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CDS
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     /product="yojH"
     /protein_id="AAA16402.1"
     /db_xref="GI:424051"
     /translation="MTMVERLEGVAQESSNGWNNAGTGHSALMELNYTPQNADGSISI
                    EKAVAINEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDNVNFLRARYAAL
                    QQSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQQKVAATRTEIGTDVNYGEITROLIAS
                    LQKKSNFSLQLSSEVRALKRKNDDNTWTVTVADLKNGTAQNIRAKFVFIGAGGAALKLL
                    QESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHIDTRVLD
                    GKRVVLFGPFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVSQVML
                    SEEDRFEALKEYYQAKKEDWRLWAGAGQRVQIIKRDAEKGGVLRIGTEVVSDQQGTIA
                    ALLGASPGASTAAPIMLNLLEKVFGDRVSSPQWQATLKAIVPSYGRKLNGDVAATERE
                    LQTSEVLGLNYDKPQAADSTPKPQLKPQPVQKEVADIAL"
     complement(34023..35666)
     /note="ABC-type ATP-dependent transport protein. Match to
     syrD from Pseudomonas syringae over most of length and
     outside ABC-family signatures."
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CDS
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     /codon_start=1
     /transl_table=11
     /product="yojI"
     /protein_id="AAA16403.1"
     /db_xref="GI:453991"
     /translation="MELLVLVWRQYRWPFISVMALSLASAALGIGLIAFINQRLIETA
                    DTSLLVLPEFLGLLLLLMAVTLGSQLALTTLGHHFVYRLRSEFIKRILDTHVERIEQL
                    GSASLLAGLTSDVRNITIAFVRLPELVQGIILTIGSAAYLWMLSGKMLLVTAIWMAIT
                    IWGGFVLVARVYKHMATLRETEDKLYTDFQTVLEGRKELTLNRERAEYVFNNLYIPDA
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ORIGIN
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Initial Score  =    77    Optimized Score    =   291    Significance     =  1.16
Residue Identity =  48%   Matches            =   356    Mismatches       =   278
Gaps           =    96    Conservative Substitutions =   96                   0
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                                         |||    ||||| ||| || ||
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17590        17600        17610        17620  17630  X 17640      17650
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              360        370        380        390        400        410        420
GAGCCGGACGACGCGTCGCTGGCAAAGCTGCGCAACGGCGTAACGCTGACGA-CGGTCCCA--CCCTGCCG
              ||||| ||| |||  ||||| ||||| ||| |||| || ||||| ||||   |||    |||||||
GATCCCTTC--AGCGT-GCTGACGGAGC-GCG-AGCTG-GATGTTCTGCACGAGCTGGCACAGGGGCTGTCA
18000        18010        18020        18030        18040        18050        18060
                     430        440        450        460        470        480
GCT---GGTATTG-AACG-TG-TGAATGAACCCAG--TGGCTGTGGCCGGCA-ACCCGCCGATTCGTGAGC
    ||      ||  ||| ||  || |||  |||     ||| || |||| ||   |||||  |||| | ||
AATAAACAGATTGCCTCGGTGTTGAATATTTCCGAGCAGCAGTAAAGTACATATTCGC--AATCTGCTGC
18070        18080        18090        18100        18110        18120        18130
                     490        500        510        520        530        540
GTAAA-TCCAT-TCCTACCA-GC-TGGCTTAAAATCACCCTT-TATGAAGGCCGCAACCGACAGGTCAGGCG
||||   ||||  ||| |||  ||  ||||| ||| ||| |   |||  || || |||| |||||  |||||
GTAAACTCAATGTCCGTCACGCGTGGC-----GGCCACCATTCTGTTCCTGCAACAAC--CGGGGCACAAT
18140        18150        18160        18170        18180        18190
              560        570        580        590        600        610
CATGACTCGGCCATGTGGCTTCCCTAC--CCTGCGACTCATTCGCTACGCCA---TG-GGCAGCTATACGC
|||| |||| ||||  |||||  | |   || |||| ||| | |||| ||||     ||  |||| |||||
AAAAATAGC-CCGATGGATTTATCATCGGGCTGAGATTTATGACAAACGCCAAAACTGCTGATGCGCTACGC
18200        18210        18220        18230        18240        18250        18260
                     620        630        640        650        660      X
T----GGACTCGCTGGCAAACGGGAATGGCGGGATGTTACCC--CTAAGGAGAACTGA
 |    |||| ||||  |||  ||| || || |||| || || ||  || ||| |||||
TTATCAGGCCTACGTGG--ATCGATCAATTATTGAATTTACACAATTTGTAGGCCGGATAAGGCGTTCAC
18270        18280        18290        18300        18310        18320        18330

GCCGCATCCGGCATAAACTAAGCGCACTTTGTCAACAG
18340        18350        18360        18370
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                                         X        10
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17660        17670        17680        17690        17700        17710        17720

                    150        160        170        180        190        200        210        220
CGATGTATT-GCCGCAGTTACCGACGCGGGCGCGCGAGCCGCCCAGCACGCTTGAAGGACTTTATCCCCGTACAGGGAG
17800        17810        17820        17830        17840        17850

                   90        100        110        120        130        140
T-CACGACAAGCCACCAG--AAGA-ACGGCCAGACGCCACCCCAGCCAACCGGGTCATACTGTTCAATAAACCCTA
17730        17740        17750        17760        17770        17780        17790

                   230        240        250        260        270        280
TCTACGGCAGCGGGACGTCTG-----GATCGCGACAGCGAGGGGCTGCTGGTCCTTGCCTGGTGTTCGTCGCCGGAGCGA
17860        17870        17880        17890        17900        17910        17920

                   290        300        310        320        330        340        350
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           Rivolta,C., Rocha,E., Roche,B., Rose,M., Sadaie,Y., Sato,T.,
           Scanlan,E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J.,
           Sekowska,A., Seror,S.J., Seror,P., Shin,B.S., Soldo,B.,
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           Viari,A., Wambutt,R., Wedler,E., Wedler,H., Weitzenegger,T.,
           Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yata,K.,
           Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and
           Danchin,A.
  TITLE      The complete genome sequence of the gram-positive bacterium
             Bacillus subtilis
  JOURNAL    Nature 390 (6657), 249-256 (1997)
  MEDLINE    98044033
REFERENCE   2 (bases 1 to 218470)
  AUTHORS    Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.
  TITLE      Direct Submission
  JOURNAL    Submitted (18-NOV-1997) I. Moszer. A. Danchin, Institut Pasteur,
             Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
             Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
             adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
             68 89 48
FEATURES             Location/Qualifiers
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                   RKLKTATIEDHIVEISLHEPAFMINDYVSAEDQLQIAEFAKRMRTNKIKQIRDGLEQR
                   FSYPQIRLALTKQVQQYD"
gene               13703. .13951
                   /gene="fer"
CDS                13703. .13951
                   /gene="fer"
                   /note="alternate gene name: ypbA"
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                    /db_xref="SWISS-PROT:P50727"
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                    VEVPEVLEEDMIDAFEGCPTDSIKVADEPFEGDPLKFE"
gene                complement(13967..14563)
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terminator          complement(13967..13982)
                    /gene="ypaA"
CDS                 complement(13991..14563)
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                    /function="unknown"
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                    /translation="MKVKKLVVVSMLSSIAFVLMLLNFPPGLPDYLKIDFSDVPAII
                    AILIYGPLAGIAVEAIKNVLQYIIQGSMAGVPVGQVANFIAGTLFILPTAFLFKKLNS
                    AKGLAVSLLLGTAAMTILMSLNYVLILPAYTWFLHSPALSDSALKTAVVAGILPFNM
                    IKGIVITVVFSLIFIKLKPWIEQQRSAHIH"
gene                complement(14669..14833)
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CDS                 complement(14669..14833)
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                    /function="unknown"
                    /codon_start=1
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                    /db_xref="SPTREMBL:O32010"
                    /translation="MKFPTGGDEPMALSPRAVFTAGFGEIPEPTVQSGWEKMEVHKRF
                    EIEFFKRFFA"
gene                15060..16676
                    /gene="serA"
CDS                 15060..16637
                    /gene="serA"
                    /EC_number="1.1.1.95"
                    /function="serine biosynthesis"
                    /codon_start=1
                    /transl_table=11
                    /product="phosphoglycerate dehydrogenase"
                    /protein_id="CAB14239.1"
                    /db_xref="GI:2634742"
                    /db_xref="SWISS-PROT:P35136"
                    /translation="MPRVLVSDKMSNDGLQPLIESDFIEIVQKNVADAEDELHTFDAL
                    LVRSATKVTEDLFNKMTSLKIVGRAGVGVDNIDIDEATKHGVIVINAPNGNTISTAEH
                    TFAMISSLMRHIPQANISVKSREWNRTAYVGSELYGKTLGIVGLGRIGSEIAQRRGAF
                    GMTVHVFDPFLTEERAKKIGVNSRTFEEVLESADIITVHTPLTKETKGLLNKETIAKT
                    KKGVRLINCARGGIDEAALLEALENGHVAGAALDVFEVEPPVDNKLVDHPLVIATPH
                    LGASTKEAQLNVAAQVSEEVLQFAKGLPVMSAINLPAMTKDEFAKIKPYHQIAGKIGS
                    LVSQCMKEPVDVAIQYEGTIAKLETSFITKALLSGFLKPRVDSTVNEVNAGGVAKER
                    GISFSEKISSSESGIDNCISVKVTGDRSTFTVATYIPHFGERIVEINGFNIDFYPTG
                    HLVYIQHQDTTGVIGRVGRIIGDNDINIATMQVGRKEKGGEAIMMLSFDRHLEDKIVK
                    ELTNVPDIVSVLIDLP"
terminator          16636..16676
                    /gene="serA"
gene                complement(16680..17447)
                    /gene="aroC"
CDS                 complement(16680..17447)
                    /gene="aroC"
                    /EC_number="4.2.1.10"
                    /function="shikimate pathway"
                    /codon_start=1
                    /transl_table=11
                    /product="3-dehydroquinate dehydratase"
                    /protein_id="CAB14240.1"
                    /db_xref="GI:2634743"
                    /db_xref="SWISS-PROT:P35146"
                    /translation="MNVLTIKGVSIGEGMPKIIIPLMGKTEKQILNEAEAVKLLNPDI
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                    VEWRVDVFEKANDREAVTKLISKLRKSLEDKLFLFTFRTHKEGGSMEMDESSYLALLE
                    SAIQTKDIDLIDIELFSGDANVKALVSLAEENNVYVVMSNHDFEKTPVKDEIISRLRK
                    MODLGAHIPKMAVMPNDTGDLLTLLDATYTMKTIYADRPIITMSAARTGLISRLSGEV
                    FGSACTFGAGEEASAPGQIPVSELRSVLDILHKNTRG"
terminator          complement(17540..17555)
                    /gene="ypuN"
gene                complement(join(17540..17555,17559..18665))
                    /gene="ypuN"
CDS                 complement(17559..18665)
                    /gene="ypuN"
                    /function="unknown"
                    /note="similar to negative regulator of sigma-X activity"
                    /codon_start=1
                    /transl_table=11
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                    /db_xref="GI:2634744"
                    /db_xref="SWISS-PROT:P35166"
                    /translation="MMKSEWNEEQIKELLSQLPAVKDHRSPQDIYKRLTMAKRKNPA
                    VRWIGPACAAIAVYIAFIISPHFFDQAQPQQKEASQENAVTKTETEDSPKAASSLDQ
                    TSPVVPEKEQDNYITVAVADADTSAIIPVSIQKTNADQTIQDMLFESSELGILDHAIT
                    IPTFIDEVEIKEKPKQKELSIRVHQPATAFSIKDDTLLKKLLESLKWSPYAFKFLS
                    DQNETGVRIGSYGTFTEISIPKQSKRSYLYQNKQGQDFLVPSNHSFDTVKEAIKEME
                    SSSQEDTTPLIQAGAVQSVTKKQKHLYMRFSKESEVDDSIAGILMIEGLLLTAKEFGF
                    TEVTFTETRTKKIGKYDISDAIFVPAAPNPISLN"
gene                complement(18601..19185)
                    /gene="sigX"
CDS                 complement(18601..19185)
                    /gene="sigX"
                    /note="alternate gene name: ypuM"
                    /codon_start=1
                    /transl_table=11
                    /product="RNA polymerase ECF-type sigma factor (sigma-X)"
                    /protein_id="CAB14242.1"
                    /db_xref="GI:2634745"
                    /db_xref="SWISS-PROT:P35165"
                    /translation="MEETFQLLVDTYHQDLYQFLFYMVKDKNQTEDLLQEVYIRVLNS
                    YHTFEGRSSEKTWLLSIARHVAIDWFRKQQTIRQRILGTFDWDTQDVRDQQLLPDELA
                    VQHENVREISCALDQCTIDQRAVIILRFIQGYSIQETAKALRFSESKVKTTQHRGLKV
                    LRKHMELREELMDDEVRMERRTDKGVVKSTSGS"
gene                complement(join(19326..19346,19389..21158))
                    /gene="resE"
terminator          complement(19326..19346)
                    /gene="resE"
CDS                 complement(19389..21158)
                    /gene="resE"
                    /function="involved in global regulation of aerobic and
                    anaerobic respiration"
                    /note="alternate gene name: ypxE"
                    /codon_start=1
                    /transl_table=11
                    /product="two-component sensor histidine kinase"
                    /protein_id="CAB14243.1"
                    /db_xref="GI:2634746"
                    /db_xref="SWISS-PROT:P35164"
                    /translation="MKFWKSVVGKLWFTILSLVLVLFILTVLLLEFIENYHVEEAEN
                    DLTQLANKVAVILENHEDQALARSITWELADNLTSIAIIQDEKNHWYSPNDKNRLSSI
                    TVEQIQHDKDLNKALKDHKKVSKRTGLSDTDTDNERLIVGVPYEKDGKKGMVFLSQSL
                    LAVKDTTKHTTRYIFLAAGIAIVLTTFFAFFLSSRVTYPLRKMREGAQDLAKGKFHS
                    IPILTQDEIGELATAFNQMGRQLNFHINALNQEKEQLSNILSMADGVITINIDGTIL
                    VNPPAERFLQAWYEQNMNIKEGDNLPPEAKELFQNAVSTEKEQMIEMTLQGRSWVL
                    LMSPLYAESHVRGAVAVLRDMTEERRLDKLREDFIANVSHELRTPISMLQGYSEAIVD
                    DIASSEDRKEIRAQIIYDESLRMGRLVNDLLDLARMESGHTGLHYEKINVNEFLEKII
                    RKFSGVAKEKNIALDHDISLTEEFMFDEDKMEQVFTNLIDNALRHTSAGGSVSISVH
                    SVKDGLKIDKDSGSGIPEEDLPFIFERFYKADRKARTRGRAGTCLGLAIVKNIVEAHN
                    GSITVHSRIDKGTTFSFYIPTKR"
gene                complement(21155..21877)
                    /gene="resD"
CDS                 complement(21155..21877)
                    /gene="resD"
                    /function="activation role in global regulation of aerobic
                    and anaerobic respiration (resA, ctaA, qcrABC, fnr)"
                    /note="alternate gene name: ypxD"
                    /codon_start=1
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gene
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                /product="two-component response regulator"
                /protein_id="CAB14244.1"
                /db_xref="GI:2634747"
                /db_xref="SWISS-PROT:P35163"
                /translation="MDQTNETKILVVDDEARIRRLLRMYLERENYAIDEAENGDEAIA
                KGLEANYDLILDLMMPGTDGIEVCRQIREKKATPIIMLTAKGEEANRVQGFEAGTDD
                YIVKPSPREVVLRVKALLRRASQTSYFNANTPTKNVLVFSHLSIDHDAHRVTADGTE
                VSLTPDKVYEFLAKTPDKVYDREKLLKEVWQYEFFGDLRTVDFTHVKRLREKLNKVS
                PEAAKKIVTVWGVGVGVKFEVGAE"
                complement(21958..23016)
                /gene="resC"
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CDS
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                complement(21958..23016)
                /gene="resC"
                /note="alternate gene name: ypxC"
                /codon_start=1
                /transl_table=11
                /product="essential protein similar to cytochrome c
                biogenesis protein"
                /protein_id="CAB14245.1"
                /db_xref="GI:2634748"
                /db_xref="SWISS-PROT:P35162"
                /translation="MGQHWNHPFYCRFFLPPRIFHHKVGCNGHAPVSNMFEFTTAFGM
                MLVLAFIILYFLYRLDPSLGLFTLSALLLJAYASMFPTDISPLIPSLQSNWLYIHVTT
                AALGQAILAISFVAGVIFLLKHVDQTKPSKKTFWLEAIMFILVTTVAFIAITSAFRLA
                GYEAAEFNWVDKSKEKSVMYEMPALVGPHQGELLTEGRMEPLVDLPALFSGRKVNTVI
                WSFGAGLVLYGALRLLIRKKRISALLHPLVKNVNLDLVDEVGYRAVSIGFPIFTLGALI
                FAMIWAQLAWTRFWGWDPKEVWALITFLFYAAYLHLRLSRGWHGEKSAWLAVIGFAII
                MFNLIFVNLVLAGLHSYA"
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gene
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                complement(23152..24780)
                /gene="resB"
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CDS
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                complement(23152..24780)
                /gene="resB"
                /note="alternate gene name: ypxB"
                /codon_start=1
                /transl_table=11
                /product="essential protein similar to cytochrome c
                biogenesis protein"
                /protein_id="CAB14246.1"
                /db_xref="GI:2634749"
                /db_xref="SWISS-PROT:P35161"
                /translation="MKQVKCECGHINPVGTVLCESCGRALQETQPPLADMRYDGSARR
                SQTNKTIIDKIWNFFSSVKVGIWLIVITLAASAFGTIFPQEAYLPPGAQADTYYKEQ
                YGTFGQLYYLLGFIHLYGSWYLLLIASTGISLVICSLDRVIPLYRALKNQGVRRSPA
                FLRRQRLFSETVTVLNGESKEKIVTLLKKKHYRIREKEGSILAEKGRFSRWGFYVNHI
                GLIIFLIGAMLRFVPGMYVDETLWVREGETAAIPGTDGKYYLKNNQFSVETYNSKTEK
                KVFADAIDRVGDGRVAKNFQTDAVLYKREGIVYGEKPKLEKVTEEDIRVNQPLRFDS
                FSVYQVDYKENQLDQMVFQLIDKKTKKSFGSLKINLLDPDSVVDLGNGYKVEIASYLP
                DFYFNQDGEPSTKTKIPNNPAFVFNIITPDKPKPGEKSFVAIQETIEGSGNNKYKLKFD
                HVETKNITGLTVRKDLTLWVLAVGGAIFMGVIQGMYWQHRRIWLHSQDGAVMVAGHT
                NKNWFGLKKDLAFILADSGLTEPVDQKELIKTQK"
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gene
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                complement(24777..25322)
                /gene="resA"
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CDS
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                complement(24777..25322)
                /gene="resA"
                /note="alternate gene name: ypxA"
                /codon_start=1
                /transl_table=11
                /product="essential protein similar to cytochrome c
                biogenesis protein"
                /protein_id="CAB14247.1"
                /db_xref="GI:2634750"
                /db_xref="SWISS-PROT:P35160"
                /translation="MDNEKKAFIHSDRHPSRNLRTRLYHLQRCICRQREYIRRSDA
                PNFVLEDTNGKRIELSDLKGKGVFLNFWCEPCKKEFPYMANQYKHFKSQGVEIVA
                VNVGESKIAVHNFMKSYGVNFPVVLDTDRQVLDAYDVSPLPTTFLINPEGKVKVVTG
                TMTESMIHDYMNLIKPGETSG"
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gene
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                complement(25454..26143)
                /gene="ypuL"
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CDS
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                complement(25454..26143)
                /gene="ypuL"
                /function="unknown"
                /note="similar to hypothetical proteins"
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                /codon_start=1
                /transl_table=11
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                /db_xref="GI:2634751"
                /db_xref="SWISS-PROT:P35159"
                /translation="MERLQKVIAHAGVASRSKAEELIKEGKVKVNGKVVTELGVKVTG
                SDQIEVNGLKVEREEPVYFLLYKPRGVISAAQDDKGRKVVTDFFKNIPQRIYPIGRLD
                YDTSGLLLLTNDGEFANKLMHPKYEIDKTYAVKVGIPPKELLRKLERGIRLEEGKTA
                PAKAKLLSLDKKKQTSIQLTIHEGRNRQVRRMFEAIGHEVIKLKREEYAFLNLRGLH
                TGDARELRLTK"
                complement(26227..26774)
                /gene="spmB"
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terminator
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                complement(26227..26241)
                /gene="spmB"
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CDS
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                complement(26235..26774)
                /gene="spmB"
                /function="required for spore core dehydration"
                /note="alternate gene name: ypuK"
                /codon_start=1
                /transl_table=11
                /product="spore maturation protein"
                /protein_id="CAB14249.1"
                /db_xref="GI:2634752"
                /translation="MEIINWLSLAMIPIIIAGILLYGTIKKVPVTYESFVGGKEGIEI
                AFSHYPLFSRNACRYNCFQIHPGALDFIMDLLKPAFSAIGIPAEVVPLALIRPISGTA
                ALGMTTDLIAVYGPDSFIGRLASVMQGSTDTTLYVLTVYFGAVGIKKMGDALKVGLLA
                DLIGVVASIIIVTLLFGSA"
                complement(26779..27369)
                /gene="spmA"
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gene
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                complement(26779..27369)
                /gene="spmA"
                /function="required for spore core dehydration"
                /note="alternate gene name: ypuJ"
                /codon_start=1
                /transl_table=11
                /product="spore maturation protein"
                /protein_id="CAB14250.1"
                /db_xref="GI:2634753"
                /translation="MVNIIWVSLTVIGLVFAMCNGTLQDVNEAVFKGAKEAITISFGL
                MSVLVFWLGLMKIAEQSGLLDIFSRMCRPFISKLFPDIPPDHPAMGYILSNLMANFFG
                LGNAATPLGIKAMEQMKKLNGNRSEASRSMITFLAVNTSCITLIPTTVIAVRMAYSSK
                TPTDIVGPSIATLISIGIGAIIIDRYFYYRRKKGR"
                complement(27357..28505)
                /gene="dacB"
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CDS
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                complement(27357..28505)
                /gene="dacB"
                /EC_number="3.4.16.4"
                /function="required for spore cortex synthesis
                (peptidoglycan biosynthesis)"
                /codon_start=1
                /transl_table=11
                /product="D-alanyl-D-alanine carboxypeptidase
                (penicillin-binding protein 5*)"
                /protein_id="CAB14251.1"
                /db_xref="GI:2634754"
                /db_xref="SWISS-PROT:P35150"
                /translation="MRIFKKAVFVIMISFLIATVNVNTAHAAIDVSAKSAIIIDGASG
                RVLYAKDEHQKRRIASITKIMTAVLAIESGKMDQTVTVSANAVRTEGSAIYLFEGQKV
                KLKDLVYGLMLRSGNDAAVAIAEHVGGSLDGFVYMNQKAEQLGMKNTRFQNPHGLDD
                HENHYSTAYDMAILTKYAMLKDYQKISGTKIYKAETMESVWKNKNKLLTMLYPYSTG
                GKTGYTKLAKRTLVSTASKDGIDLIAVTINDPNDWDDHMKMFNVFEHYQTYLIAKKG
                DIPKLKGTFYESKAFIKRDITYLLTEEEKENVKINTTLLKPKKAWEKDASKIPDIVGH
                MEIMFNDATIAKVPIYYENERHQKPKKQFFETFKSIFLNAAGGAKWSI"
                complement(28601..28621)
                /gene="ypuI"
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terminator
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                complement(28601..28621)
                /gene="ypuI"
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gene
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                complement(28628..29167)
                /gene="ypuI"
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CDS
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                complement(28628..29167)
                /gene="ypuI"
                /function="unknown"
                /note="similar to hypothetical proteins from B. subtilis"
                /codon_start=1
                /transl_table=11
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gene
CDS
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     /protein_id="CAB14252.1"
     /db_xref="GI:2634755"
     /db_xref="SWISS-PROT:P35156"
     /translation="MKEAKCERQIHEGKIPNEMGHSIVRAQTQKTGEFLSMVVNTVND
     YLNQTLESLQAELPIEKGYCCDVLSTLRRMAVFCEGGAEACRRLLMQEPFQEARAEK
     TLYNVYHQCIEEFFMPKKDTWCENSRASYTGVSAIEFYHAVPASLEQLLLPLSAAFLK
     MREELAHYEASGSSMAPIR"
     /gene="ypuH"
complement(29222. .29815)
complement(29222. .29815)
     /gene="ypuH"
     /function="unknown"
     /note="similar to hypothetical proteins"
     /codon_start=1
     /transl_table=11
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gene
CDS
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     /protein_id="CAB14253.1"
     /db_xref="GI:2634756"
     /db_xref="SWISS-PROT:P35155"
     /translation="MGLDIVNWKAIVEALLYAAGDEGLTKKQLLTVLEIEEPELNTIM
     ADVADEYRGDTRGIELIEYADTYMLSTKKDFAPYLKKLIEVPSKGLSQASLEVLAIVS
     YKQPTRAEIEIRGVKSERILHSLVAKALLCEVGRADGPGRAILYGTTPFLEQFGL
     KTLDELPPLPENAEEDVLQEEADLFENFNQTFEDIK"
     /gene="ypuG"
complement(29805. .30560)
complement(29805. .30560)
     /gene="ypuG"
     /function="unknown"
     /note="similar to hypothetical proteins"
     /codon_start=1
     /transl_table=11
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gene
CDS
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     /protein_id="CAB14254.1"
     /db_xref="GI:2634757"
     /db_xref="SWISS-PROT:P35154"
     /translation="MEEYQVKIDTFEGPLDLLHLINRLEIDIYDIPVAKITEQYLLY
     VHTMRVLELDIASEYLVMAATLLSIKSRMLLPKQEEELFEDELLEEDPRELIEKLI
     EYRKYKDAAKDLKEREEEROKSFTKPPSDLSEYAKEVKQSEQKLSVTVYDMIGAFQKV
     LKRKKINRPMETTITRQDIPIEARMNEIVHSLKSRGTRINFMDLFYEQKEHLVVTFL
     AVLELMKNQLVLIEQEHNFSDIYITGSESIHGA"
     /gene="ypuF"
30841. .31365
30841. .31365
     /gene="ypuF"
     /function="unknown"
     /codon_start=1
     /transl_table=11
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gene
CDS
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     /protein_id="CAB14255.1"
     /db_xref="GI:2634758"
     /db_xref="SWISS-PROT:P17617"
     /translation="MYPKAYIDYLVEFHATRDYFECHEILEEYWKEDPPKKKRYWVG
     FIQLAVALYIHRRQNTAGAKRLMANSIRILQAEHRAVEDLGLDHGRLLELMQSVYEQI
     ETVSAYKSIILPIKDEKLEEACRIECRKKKYTWGQPSALSNIFLIDKHRLRDRTDVIR
     EREKEIERRKKSRD"
```

terminator
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complement(31355. .31378)
     /gene="ribT"
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gene
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complement(join(31355. .31378,31379. .31753))
     /gene="ribH"
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CDS
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complement(31379. .31753)
     /gene="ribH"
     /gene="ribT"
     /function="riboflavin biosynthesis"
     /note="alternate gene name: ribD"
     /codon_start=1
     /transl_table=11
     /product="reductase"
     /protein_id="CAB14256.1"
     /db_xref="GI:2634759"
     /db_xref="SWISS-PROT:P17622"
     /translation="MLIRYKKSFEKIAMGLLSFMPNEKDLKQLQQTIKDYETDTDRQL
     FLWKEDEDIVGAIGVEKKDSEVEIRHISVNPSHRHQGIGKQMMDALKHLFKTQVLVPN
     ELTQSFFERCGQGQDQDISYNN"
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gene
CDS
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     /function="riboflavin biosynthesis"
     /codon_start=1
     /transl_table=11
     /product="riboflavin synthase (beta subunit)"
     /protein_id="CAB14257.1"
     /db_xref="GI:2634760"
     /db_xref="SWISS-PROT:P11998"
     /translation="MNIIQGNLVGTGLKIGIVVGRFNDFITSKLLSGAEDALLRHGVD
     TNDIDVAWVPGAFEIPFAKKMAETKKYDAIITLGTVIRGATTHYDVCNEAAKGIAQ
     AANTTGVPVIFGIVTTENIEQAIERAGTKAGNKGVDCAVSAIEMANLNRSFE"
     /gene="ribA"
complement(32363. .33559)
complement(32363. .33559)
     /gene="ribA"
     /EC_number="3.5.4.25"
     /function="riboflavin biosynthesis"
     /codon_start=1
     /transl_table=11
     /product="GTP cyclohydrolase II and
     3,4-dihydroxy-2-butanone 4-phosphate synthase"
     /protein_id="CAB14258.1"
     /db_xref="GI:2634761"
     /db_xref="SWISS-PROT:P17620"
     /translation="MFHPIEEALDALKKGEVIIVDDDRENEGDFVALAEHAIPEVI
     NFMATHGRGLICTPLSEEIADRLDLHPMVEHNTDSHHTAFTVSIDHRETKTGISAQER
     SFTVQALLDSKSVPSDFQRPGHIFPLIAKKGGVLKRAGHTEAAVDLAEACGSPAGVI
     CEIMNEDGTMARVPELIEIAKKHQLKMITIKDLIQYRNLTTLVEREVDITLPTDFGT
     FKVYGYTNEVDGKEHVAFVMGDVPFGEEPVLVRVHSECLTGDVFGSHRCDCGPQLHAA
     LNQIAAEGRGVLLYLRQEGRGIGLINKLAYKLQEQGYDTVEANEALGFLPDLRNYGI
     GAQILRDLGVRNMKLLTNNPRKIAGLEGVGLSISERVPLQMEAKEHNKYLQTKMNKL
     GHLLHF"
     /gene="ribB"
complement(33574. .34221)
complement(33574. .34221)
     /gene="ribB"
     /EC_number="2.5.1.9"
     /function="riboflavin biosynthesis"
     /codon_start=1
     /transl_table=11
     /product="riboflavin synthase (alpha subunit)"
     /protein_id="CAB14259.1"
     /db_xref="GI:2634762"
     /db_xref="SWISS-PROT:P16440"
     /translation="MFTGIIEETGTIESMKKAGHAMALTIKCSKILEDVHLGDSIAVN
     GICLTVTDFTKNQFTVDVMPETVKATSLNDLTKGSHVNLERAMAANGRPGGHFVSGHV
     DGTAEITRIEEKSNAVYDLKMDPSLTKTLVLKGSITVDGVSLTIFGLTEDTVTISLI
     PHTISETIPSEKTIGSKVNIECDMIGKYMYRFLHKANENKTQQTITKAFLSENGF"
     /gene="ribG"
complement(34232. .35317)
complement(34232. .35317)
     /gene="ribG"
     /function="riboflavin biosynthesis"
     /codon_start=1
     /transl_table=11
     /product="riboflavin-specific deaminase"
     /protein_id="CAB14260.1"
     /db_xref="GI:2634763"
     /db_xref="SWISS-PROT:P17618"
     /translation="MEEYMKLALDLAKQGEGQTESNPLVGAVVVKDGQIVGMGAHLK
     YGERAHEVHAIHMAGAHAEGADIYVTLEPCSHYGKTPPCAELIINSGIKRVFVAMRDP
     NPLVAGRGISMKEAGIEVREGILADQAERLNEKFLHFMRTGLPYVTKAAASLDGKI
     ATSTGDSKWITSEAARQDAQQYRKTHQSILVGVGTVKADNPSLTCRLPNVTKQPVRVI
     LDTVLSIPEDAKVICDQIAPTWIFTTARADEEKKKRLSAFGVNIFTLETERIQIPDVL
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gene
CDS

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terminator       complement(35679..35705)
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CDS              complement(35710..36054)
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terminator       complement(36262..36282)
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CDS              complement(36289..36843)
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CDS              complement(38116..38319)
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gene             complement(39298..39764)
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CDS              complement(39333..39764)
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                 THNISGITDEMYLNALMTAGVKDAKYVTAPFEVSGTAALTGLIKAYEVSSDEAISED
                 VKQVANQELVTSELGDKIGNENAAALIAKIKEEFAKNGVPDNKADIEKQVDDAASDL
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terminator       40897..40912
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CDS              complement(40919..42238)
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                 /db_xref="SWISS-PROT:P23630"
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                 EAHTHDYITTGQEDSKFGFDLHNGQTERAIEQVLGEHIOLGLVHCIGSOIFDTAGF
                 VLAARKIFFKLDEWRDSYSFVSKVLNLGGGFGIRYTEDDEPLHATEYVEKIIEAVKEN
                 ASRYGFDIPEIWIEPGRSLVGDAGTLYTVGSQKEVPGVRQYVAVDGGMNDNIRPALY
                 QAKYEAAAANRIGEAHDKTVSIAGKCCESGDMLIWDIDLPEVKEGDLLAVFCTGAYGY
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gene             complement(42344..43822)
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CDS              complement(42344..43822)
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                    TDQVLSGLVAVIVEGAGFAFIIDVRSYPGRNPEEPDTEKVVRGARDGFVENIVVNTAL
                    LRRIRDERLRVKMTKVGERSKTDLSICYIEDIADPDLVEIVEKEIASIDVDGLTMAD
                    KTVEEFIVNQSYNPPFLVRYTERPDVAANHVLEGHVIIVDTSPSVIITPTTLFFHVQ
                    HAEEYRQAPSVGTFLRWVRFFGILASTLFLFPIWFLFVLQPDLLPDNMKFIGLNKDTHI
                    PIILQIFLADLGIEFLRMAAIHTPALSTAMGLIAAVLIGQIAIEVGLFSPEVILYVS
                    LAAIGTFTTPSYELSLATNEPSCPHDTRCFISYKRARHRIYSANYAMASIKSLQTPYL
                    WPLIPFNGKALMQVLVRTAKPGAKVRPSIVHPKNRLRQPTNS"
gene            complement(43773..44744)
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CDS             complement(43773..44744)
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                    STRSGAELVKLIASAPYDPVFVMFDDSGLQGEGPGEAALIYVATHPSIEVLGVIAVAS
                    KTHQAEWTRVDVSIDRNGEITEYGVDVKVGEREFDDHRMSGDTVYCLDKLDLPLTIGIG
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gene            complement(44746..45762)
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CDS             complement(44746..45762)
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                    ATSTVTGSGAVVISQTPGDIQITSATVGKVSDLGITDPFDMGSAMAPAAADTIKQHFK
                    DLNRTADDYDLILTGDLSGVGSPIVKDILKEDGYPVGTKHDDCGLLIYTPDQQVFAGG
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gene            complement(45775..46227)
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CDS             complement(45775..46227)
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                    /db_xref="GI:2634777"
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gene            complement(46239..46664)
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CDS             complement(46239..46664)
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gene            complement(46674..47276)
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CDS             complement(46674..47276)
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gene            complement(47398..48165)
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CDS             complement(47398..48165)
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                    /note="alternate gene name: spoIIAC"
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                    DDGTVKVSRSLKELGNKIRRAKDELSKTLGRVPTVQETADHLEIEAEDVVLAQEAVRA
                    PSSIHETVYENDGPITLLDQIADNSEEKWFDKIALKEAISDLEEREKLIVYLRYKD
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gene            complement(48177..48617)
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CDS             complement(48177..48617)
                    /gene="spoIIAB"
                    /function="binding to sigma-F (SpoIIAC) in the presence of
                    ATP before septation; phosphorylation of SpoIIAA (stage II
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                    /transl_table=11
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gene            complement(48614..48967)
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CDS             complement(48614..48967)
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                    /function="binding to SpoIIAB in the presence of ADP
                    selectively in the forespore (stage II sporulation)"
                    /codon_start=1
                    /transl_table=11
                    /product="anti-anti-sigma factor (antagonist of SpoIIAB)"
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gene            complement(49063..50232)
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CDS             complement(49063..50232)
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                /note="alternate gene name: yqkN"
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                LKPFDRTVMNELKDCGLDVISIGKISDIYDGEGITSSRRTVSNMDGMDKVIDYLGEDF
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gene
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CDS
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terminator   complement(84681..84706)
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             complement(84717..85937)
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terminator   complement(89613..89636)
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terminator   complement(89648..90763)
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                       KSGYAGHASNLGGIIAREIAGLNIPSYIVDPVVVDEMSVLAKVSGMEPEIERKSIFD
                       ALNQKAVARKAAASLGKRYENMKMIITHMGGGITIGVHDRGRVVDVNNGLHGEGPFSP
                       ERAGTVPAGDLVDLCFSGEYTKEEIMKKLVGTGLLGLYGTNDAVKVEQMIQGGDEKA
                       RFIYDAMAYQVAKEIGAASAALKGEVEAIVLTGLAYGKSFVSAIRSYIDWISDVLVY
                       PGENELQSLAQGALRVLQGEEQSKQYRIE"
     gene              complement(106635..107729)
                       /gene="yqiT"
     CDS               complement(106635..107729)
                       /gene="yqiT"
                       /function="unknown"
                       /note="similar to leucine dehydrogenase"
                       /codon_start=1
                       /transl_table=11
                       /protein_id="CAB14339.1"
                       /db_xref="GI:2634842"
                       /db_xref="SWISS-PROT:P54531"
                       /translation="MELFKYMEKYDYEQLVFCQDEQSGLKAIIAIHDTTLGPALGGTR
                       MWTYENEEAAIEDALRLARGMTYKNAAAGLNLGGGKTVIIGDPRKDKNEEMFRAFGRY
                       IQGLNGRYITAEDVGTTVEDMDIIHDETDYVTGISPAFGSSGNPSPVTAYGVYRGMKA
                       AAKAAFGTDSLEGKTIAVQGVGNVAYNLCRHLHEEGANLIVTDINKQSVQRAVEDFGA
                       RAVDPDDIYSQDCDIYAPCALGATINDDTIKQLKAKVIAGAANNQLKETRHGDQIHEM
                       GIYYAPDVINAGGVINVADELYGNAERALKKVEGIYGNIERVLEISQRDGIPAYLA
                       ADRLAEERIERMRRSRSQFLQNGHSVLSRR"
     gene
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gene          complement(107741..108640)
              /gene="yqiS"

CDS           complement(107741..108640)
              /gene="yqiS"
              /function="unknown"
              /note="similar to phosphate butyryltransferase"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14340.1"
              /db_xref="GI:2634843"
              /db_xref="SWISS-PROT:P54530"
              /translation="MKLKDLIGKASITKNKTIAVAHAEDEVIRAVKLAAEHLSARFL
              LTGDSKKLNELTSSMOGHQVEVIVHANTPEESAKLAVRAVHIKTADVLMKGNVPTSVLL
              KAVLNRQEGLRSASVLSHVAVFDIPDFDRLMFVTDSAMNIAPSLEELRQILQNAHVHA
              HAVGNNMPKAAALAAVETVNPKMEATVNAALAQMYKRGQIKGCIVDGPLALDNAVSQ
              IAAAQKKISGDVAGNPDILLVPTIEAGNILYKSLIYFAKASVAAVTGAKAPIALTSR
              ADSAENKLYSIALACASEEYTH"

gene          complement(108765..110843)
              /gene="yqiR"

CDS           complement(108765..110843)
              /gene="yqiR"
              /function="unknown"
              /note="similar to transcriptional regulator
              (sigma-L-dependent)"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14341.1"
              /db_xref="GI:2634844"
              /db_xref="SWISS-PROT:P54529"
              /translation="MQKVLIVGAGKRGTALLHILIKTAIIDIIAVVDKDPEAPGLKEA
              EQYGIAVSSDWKPYIQQKPDIVIHTGDQAVFDELLQRKHEDTIVMPGKMAYIVFQLM
              EEKQHLIQMLKEQTYKYDRIFNSTHDGMIFDINEEIILFNHMAEKMVGKKREEVIGR
              PIKEVIPSTKMPRRILKTRVPEYNQKQLLGDHLQIVTTRLPFIDEGGRLLGALCVFKDI
              TDAVELAEAEVKNLKQVRTMLEAIIQSSDEAISVVDENGIGLLINKAYTKMTGLSEKEV
              IGKPANTDISEGESMHLKVLETRRPVRGVRMKVGPNEKEVIVNVAPVIVDGILKGSVG
              VIHDVSEIKMLTAELNRARQIIRTLEAKYTPDDIIGKSEQMLVALEQAKLGAKTPATI
              LLRGESGTGKELFAHAIHNESDRKYNKFIRVNCAALSENLLESELFGYEDGAFSGAKR
              GGKKGLFEEANNGSIPLDEIGELTQNMQAKLLRVLQEKEIVRVGGTKAIPVNVRVIAA
              TNVNIEKAMADGTFREDLYXRINRYPISIPPLRQRLEDIEALSVRLIQKINRDYGRNV
              KGLSQQALRALSAYHWPGVRELENVLGRAMIFLNPHMEWIEKDHLPVFELEQKENDT
              DQGTGFDFPDIEGEKLSVAVEKFEAHLIQQTLEKHFNRRTKAKALGVSIRNLYYKMD
              KYGLANEGMQ"

gene          110996..111232
              /gene="yqzF"

CDS           110996..111232
              /gene="yqzF"
              /function="unknown"
              /codon_start=1
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              /protein_id="CAB14342.1"
              /db_xref="GI:2634845"
              /db_xref="SPTREMBL:O32015"
              /translation="MSRLLALLILVIPGAISALGIKLMRDTLFGHTIKPFSALWLQGL
              SGFIFFAIGLYVLSGAAYTASRGLPDLGIITSAEIAERAKDLVRAADLPLLVDTGFGGVLN"

gene          complement(111243..112179)
              /gene="yqiQ"

terminator    complement(111243..112179)
              /gene="yqiQ"

CDS           complement(111274..112179)
              /gene="yqiQ"
              /function="unknown"
              /note="similar to phosphoenolpyruvate mutase"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14343.1"
              /db_xref="GI:2634846"
              /db_xref="SWISS-PROT:P54528"
              /translation="MSWIVNKQSSQEELAGRFRKLMSAPDILQIPGAHDGMAALLAKE
              AGFSAIYLSGAAYTASRGLPDLGIITSAEIAERAKDLVRAADLPLLVDTGFGGVLN
              AARTARRMLEARVAAVQMEDQQLPKKCGHLNGKQLYPIKEMAQKIKAIKQAAPSLIVV
              ARTDARAQEGLDAAIKRSEAYIEAGADAIFPEALQAENEFRQFAERIPVPLLANMTEF
              GKTPYYRADEFEDMGFHMVIYPVTSLRAAAKACAERMFGLMKEHGSQKEGLHDMQTRKE
              LYDTISYYDYEALDKTIAKTVLPDE"

gene          complement(112197..113615)
              /gene="mmgE"

CDS           complement(112197..113615)
              /gene="mmgE"
              /function="unknown"
              /note="alternate gene name: yqiP"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14344.1"
              /db_xref="GI:2634847"
              /db_xref="SWISS-PROT:P45859"
              /translation="MPKTDRVIEEITDVVLEKEITSAEAYTAGHVLLDTLGCGILAL
              RYPECTKLLGPIVPGTTVVPNGSKVPGTSYVLDPVRAAFNIGCMIRWLDYNDTWLAAEW
              GHPSDNLGGILAAADYVSRVRLSEGKEPLTVRDVLEMMIKAHEIQGVLALENSLNRVG
              LDHVLFVKVATTAVAAKLLGGGREEIKNALSNAWIDNAALRTYRHSPNTGSRKSWPAG
              DATSRGVHLALMSLKGEMGYPTALSAPGWGFQDVLFNKKEIKLKLARPLDAYVMENVLFK
              VSYPAEFHAQTAEASAVILHPQVKNRIDEIDRVVIRTHESAIRIIDKGPLHNPADRD
              HCLQYITAIGLLFGDITAQHYEAETANDPRIDKLRDKMEVTENKTYTEDYLKPDKRSI
              SNAVQVHFKDGTSTEMVECEFPLGHRFRREEAVPKLLEKFSDNLKTHFPDKQHKHIYE
              RCTSYETLQTMRVNEFVDMFCM"

gene          complement(113630..114748)
              /gene="mmgD"

CDS           complement(113630..114748)
              /gene="mmgD"
              /EC_number="4.1.3.7"
              /note="alternate gene name: yqiO"
              /codon_start=1
              /transl_table=11
              /product="citrate synthase III"
              /protein_id="CAB14345.1"
              /db_xref="GI:2634848"
              /db_xref="SWISS-PROT:P45858"
              /translation="MEEKQHYSPGLDGVIAAETHISYLDTQSSQILIRGYDLIELSET
              KSYLEVHLLEGRLPEESEMETLERKINSASSLPADHLRLLELLPEDTHPMDGLRTG
              LSALAGYDRQIDDRSPSANKERAYQLGKMPALTAASYRIINKEPILPQTLSYSAN
              FLYMTGKLPSSLEEQIFDRSLVISEHEMPNSTFAARVIASTHSDLYGALTGAVASL
              KGNLHGGANEAVMLLLEAKTTSDFEQLLQTKLKRKEIMGFGHRVYMKKMDPRALMM
              KEALQQLCKAGDHRLYEMCEAGERLMEKEKGLYPNLDYYAAPVYWMLGIPIPLYTPI
              FFSARTSGLCAHVIEQHANNRLFRPRVSYMGPRYQTKS"

gene          complement(114782..115918)
              /gene="mmgC"

CDS           complement(114782..115918)
              /gene="mmgC"
              /EC_number="1.3.99.-"
              /note="alternate gene name: yqiN"
              /codon_start=1
              /transl_table=11
              /product="acyl-CoA dehydrogenase"
              /protein_id="CAB14346.1"
              /db_xref="GI:2634849"
              /db_xref="SWISS-PROT:P45857"
              /translation="MHVTQEQVMRKMVRDFARKEIAPAAEIMEKTDEFPFQLIKKMG
              KHGLMGIPVPEOYGGAGADVVSYLAIHEISRISAAVGVILSVHTSVGTNPILFYFGNE
              EQKMKYIPNLASGDHLGAFALTEPHSGSDAGSLRTTAIKKNGKYLLNGSKIFITNGGA
              ADIYITFALTAPDQGRHGISAFIVEKNTPGFTVGKKERKIGLYGSNTTELIFDNAEVP
              EANLLGKEGDGFHIAMANLNVGRIGIAAQLALGIAEAALEHAVDYAKORVQFGRPIAAN
              QGISFKLADMATRAEAARHLVYHAADLHNRGLNCGKEASMAKQFASDAAVKALDAVQI
              YGGYGYMKDYPVERLLRDAKVTQIYEGTNEIQRLLISKYLLGGT"

gene          complement(115946..116680)
              /gene="mmgB"

CDS           complement(115946..116680)
              /gene="mmgB"
              /EC_number="1.1.1.157"
              /function="(butyrate/butanol-producing pathway)"
              /note="alternate gene name: yqiM"
              /codon_start=1
              /transl_table=11
              /product="3-hydroxybutyryl-CoA dehydrogenase"
              /protein_id="CAB14347.1"
              /db_xref="GI:2634850"
              /db_xref="SPTREMBL:O32016"
              /translation="MKRLKKQLARDAEKGKRTETEVKSVINRISISQTLEEABADIV
              IEATAENMAAKTEMFKTLDRICPHTILASNTSSLPITEIAAVNRPQRVIGMHFMNP"
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              VPVMKLVEVIRGLATSEETALDVMALAEKMGKTAVEVNDFPGFVSNRVLLPMINEAIY
              CVYEGVRTEAIDEVMKLGMNHPMGPLALADFIGLDTCLSIMEVLHSGLGDSKYRPCPL
              LRKYVKAGWLGKKSGRGFYDYEEKTS"
gene          /gene="mmgA"
              complement(116729..118011)
              /gene="mmgA"
terminator    complement(116729..116742)
              /gene="mmgA"
CDS           complement(116830..118011)
              /gene="mmgA"
              /EC_number="2.3.1.9"
              /note="alternate gene name: yqiL"
              /codon_start=1
              /transl_table=11
              /product="acetyl-CoA acetyltransferase"
              /protein_id="CAB14348.1"
              /db_xref="GI:2634851"
              /db_xref="SWISS-PROT:P45855"
              /translation="MRKTVIVSAARTPFGKFGGVLKEVKAAELGGIVMKEALQQAGVS
              GDDVEGNVMGMVVQAGSGQIPSRQAARLAGMPWSVPSETLNKVCASGLRAVTLCDQMI
              RAQDADILVAGGMESMSNIPYAVPAGRWGARMGDGELRDLMVYDGLTCARFDEVHMAVH
              GNTAAKEYAISRREQDEWALRSHARAKAADEGKFQDEIVPVNWIGRKGKPNVVDKDE
              AIRRDTSLDQLAKLAPIYASDGSITAGNPGVNDGAGAFVLMSEEKAAELGKRPLATI
              LGFSTTGMPAHELAAAPGFAINKLLKKNGLTVQDIDLFEVNEAFASVVLTCEKIVGFD
              LEKVNVNGGAIALGHPIGASGARIMLTLVYELKRRGGGLGVAAICSGAAQGDAVLVQV
              H"
gene          /gene="yqiK"
              complement(118108..118868)
              /gene="yqiK"
terminator    complement(118108..118126)
              /gene="yqiK"
CDS           complement(118149..118868)
              /gene="yqiK"
              /function="unknown"
              /note="similar to glycerophosphodiester phosphodiesterase"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14349.1"
              /db_xref="GI:2634852"
              /translation="MTKIFPHRGASGQFPENTMLAFEKGIEAGADGIELDVQLTKDGR
              IVIHDERLNRTTSLKGFVKDTAYDEVKTANAAAGHDQAYSDIKVPLLEDVLSWAVKK
              DFLINIELKNSVIRYEGMEEKVLEAVKRFNVEDRVILSTFNHDSLALCARLAPHIERA
              VLTSDVLYQADRYTASIPASGYHPKINSPGVTDEVLKKMRNGLLIKVRPYTVNRPEDMK
              RLIEAGADRMFTDFPERLRHC"
gene          /gene="yqiI"
              complement(118947..119567)
              /gene="yqiI"
CDS           complement(118947..119567)
              /gene="yqiI"
              /function="unknown"
              /note="alternate gene name: yqiI
              similar to N-acetylmuramoyl-L-alanine amidase"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14350.1"
              /db_xref="GI:2634853"
              /db_xref="SPTREMBL:O32017"
              /translation="MRMLWRSLALCGLALTLAPCAQAEPIEGKTVYIDAGHGGEDSG
              AVGNGLFEKDINLPVSEHVTDKLKEEGANPVASRSDDHFLTLEERVAKASANQADLFV
              SIHVNSGVASASGTETYPQSDYEGENSRRLASDIQSQLVSSLQTRDRGVKESDFYVIT
              YSQMPSVLAELGFITNSSDADKLGSEEYQQKAADAIVNGIDSYYDQ"
gene          /gene="yqiH"
              complement(119582..119875)
              /gene="yqiH"
CDS           complement(119582..119875)
              /gene="yqiH"
              /function="unknown"
              /note="alternate gene name: yzpA
              similar to lipoprotein"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14351.1"
              /db_xref="GI:2634854"
              /db_xref="SWISS-PROT:P40770"
              /translation="MKQVLLLFTALFLSGCSVASADDSVPRFTEEGKYIGSADPHTI
              AVSLNGEETMIQVPKDKRDECESLPDQTHVLVKYTKKDNGTLQLEDIQLRKTS"
gene          120407..121557
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CDS           /gene="yqiG"
              120407..121525
              /gene="yqiG"
              /function="unknown"
              /note="similar to NADH-dependent flavin oxidoreductase"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14352.1"
              /db_xref="GI:2634855"
              /db_xref="SWISS-PROT:P54524"
              /translation="MNPKYKPLFEPTTFKSGVTINNRIAVAPMTHYASNEDGTISEAE
              LDYIIPRSKEMGMVITACANVTPDGKAFPGQOPAIHDDSNIPGLKKLAQAIOQAGAKAV
              VQIHHGGIECPSELVPQQDVVGPSDVFDNGKQIARALTEEEVENIVKAFGEATRRAIE
              AGFDGVEIHGANGYLIQQFYSPKTNQRTDRWGGSDEKRLAFPLAIVDEVKKAASEHAK
              GAFLVGYRLSPEEPETPGLTMETYTLVDALGDKELDYLHISLMDVNSKARRGADPTR
              TRMDLLNERVGNKVFLIAVGSIHSADDALAVIENGIPLVAMGREILVDPNWTVKVKEG
              REKQIETVIKGTDKEKYHLPEPLWQAIVNTQGWVPYKD"
terminator    121534..121557
              /gene="yqiG"
gene          complement(122041..122844)
              /gene="spo0A"
CDS           complement(122041..122844)
              /gene="spo0A"
              /function="central role in the initiation of sporulation
              (negative regulation of abrB, kinA, kinC, spo0A; positive
              regulation of spoIIA, spoIIE, spoIIG) (stage 0
              sporulation)"
              /note="alternate gene name: spo0C, spo0G, spoIIL, sof-1"
              /codon_start=1
              /transl_table=11
              /product="two-component response regulator"
              /protein_id="CAB14353.1"
              /db_xref="GI:2634856"
              /db_xref="SWISS-PROT:P06534"
              /translation="MEKIKVCVADDNRELVSLLSEYIEGQEDMEVIGVAYNGQECLSL
              FKEKDPDVLVLDIIMPHLDGLAVLERLRESDLKKQPNVIMLTAFGQEDVTKKAVDLGA
              SYFILKPFDMENLVGHIRQVSGNASSVTHRAPSSQSSIIRSSQPEPKKKNLDASITSI
              IHEIGVPAHIKGYLYLREAISMVYNDIELLGSITKVLYPDIAKKFNTTASRVERAIRH
              AIEVAWSRGNIDSISSLFGVTVSMTKAKPTNSEFIAMVADKLRLEHKAS"
gene          complement(123101..124397)
              /gene="spoIVB"
terminator    complement(123101..123119)
              /gene="spoIVB"
CDS           complement(123120..124397)
              /gene="spoIVB"
              /function="intercompartmental signalling of pro-sigma-K
              processing/activation in the mother-cell; essential for
              spore cortex and coat formation (stage IV sporulation)"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14354.1"
              /db_xref="GI:2634857"
              /db_xref="SWISS-PROT:P17896"
              /translation="MPDNIRKAVGLILLVSLLVSGLCKPLKEYLLIPTQMRVFETQTQ
              AIETSLSVNAQTSRSSEAFTVKKDPHEIKVTGKKSGESELVYDLAGFPIKKTKVHVLP
              DLKVIPGGQSIGVKLHSVGLVGFHQINTSEGKKSPGETAGIEAGDIIIEMNGQKIEK
              MNDVAPFIOKAGKTGESLDLLIKRDKQKIKTKLIPEKDEGEGKYRIGLYIRDSAAGIG
              TMTFYEPKTKKYGALGHVISDMDTKKPIVVENGEIVKSTVTSIEKGTGNPGEKLARF
              SSERKTIGDINRNSPFGIFGTLHQPIQNNISDQALPVAFSTEVKKGPAEILTVIDDDK
              VEKFDIEIVSTTPQKFPATKGMVLKITDPRLLKETGGIVQGMSGSPIIQNGKVIGAVT
              HVFVNDPTSGYGVHIEWMLSEAGIDIYGKEKAS"
gene          complement(124553..126302)
              /gene="recN"
terminator    complement(124553..124571)
              /gene="recN"
CDS           complement(124572..126302)
              /gene="recN"
              /function="DNA repair and genetic recombination"
              /codon_start=1
              /transl_table=11
              /protein_id="CAB14355.1"
              /db_xref="GI:2634858"
              /db_xref="SWISS-PROT:P17894"
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/translation="MLAELSIKNFAIIEELTVSFERGLTVLTGETGAGKSIIIDAISL
LVGGRGSSEFVRYGEAKAELEGLFLLESGHPVLGVCAEQGIDVSDEMIVMRRDISTSG
KSVCRVNGKLVTIASLREIGRLLLDIHGGDHNQLLMEDENHLQLLKFAGAEVESALK
TYQEGYQRYVKLLKQLSESEQEMAHCLDLIQFQLEEIESAKLELNEDELQEERQ
QISNFEKIYESLQNAYNALRSEQGGLDWVGMASAQLEDISDINEPLKKMSESVSNSYY
LLEDAFFQMRMRMLDELEFDPERLNYIETRLNEIKQLKRKYGATVEDILEYASKIEEEI
DQIENRDSHLQSLKKELDSVGKDVAVEAANVSQIRKTWAKKLADEIHRELKSLYMEKS
TFDTEFKVRTASRNEEAPLVNGQPVQLTEQGIDLVKFLISTNTGEPLKSLSKVASGGE
LSRVMLAIKSIFSSQQDVTSIIFDEVDTGVSGRVAQAIAEKIHKVSIGSQVLCITHLP
QVAAMADTHLYIAKELKDGRTTTRVKPLSKQEKVAEIERSIAGVEVTDLTKRHAKELL
KQADQVKTTG"
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gene        complement(126339..126788)
            /gene="ahrC"
CDS         complement(126339..126788)
            /gene="ahrC"
            /function="negative regulation of arginine biosynthesis
            and positive regulation of arginine catabolism (roc
            operons)"
            /codon_start=1
            /transl_table=11
            /product="transcriptional regulator"
            /protein_id="CAB14356.1"
            /db_xref="GI:2634859"
            /db_xref="SWISS-PROT:P17893"
            /translation="MNKGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRD
            IKELHLVKVPFNNGSYKYSLPADQRFNPLSKLKRALMDAFVKIDSASHMIVLKTMPGN
            AQAIGALMDNLDWDEKMGTICGDDTILICRTPEDTEGVKNRLLELL"
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gene        complement(126923..127732)
            /gene="yqxC"
CDS         complement(126923..127732)
            /gene="yqxC"
            /function="unknown"
            /note="alternate gene name: yqiF
            similar to hemolysin-like"
            /codon_start=1
            /transl_table=11
            /protein_id="CAB14357.1"
            /db_xref="GI:2634860"
            /db_xref="SWISS-PROT:P19672"
            /translation="MTSKKERLDVLLVERGLAETREKAKRAIMAGIVYSNENRLDKPG
            EKIDRDLPLTVKGNPLRYVSRGGLKLEKALKEFPVSVKDKIMIDIGSSTGGFTDCALQ
            NGAKQSVAVDVGVNQLAWKLRQDERVVMERFNRYATPADFTKGWMPEFATIDVSFIS
            LRLILPVLRTLLVPGSDCMALVKRQPFEAGRESVGKKGIVRDPKVHADVLKRMISFSAA
            EGYICKGLSFSPITGGDGNIEFLLQFALAGRGTGRPGTAGRRDHARCRRST"
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gene        complement(127729..129630)
            /gene="yqiE"
CDS         complement(127729..129630)
            /gene="yqiE"
            /function="unknown"
            /note="similar to hypothetical proteins"
            /codon_start=1
            /transl_table=11
            /protein_id="CAB14358.1"
            /db_xref="GI:2634861"
            /db_xref="SWISS-PROT:P54523"
            /translation="MDLLSIQDPSFLKNMSIDELEKLSDEIRQFLITSLSASGGHIGP
            NLGVVELTVALHKEFNSPKDKFLWDVGHQSYVHKLLTGRGKEFATLRQYKGLCGFPKR
            SESEHDVWETGHSSTSLSGAMGMAAARDIKGTDEYIIPIIGDGALTCGMALEALNHIG
            DEKKDMIVILNDNEMSIAPNVGAIHSMLGRTAGKYQWVKDELEYLFKKIPAVGGKL
            AATAERVKDSLKYMLVSGMFFEELGFTYLGPVDGHSYHELIENLQYAKKTGPVLLHV
            ITKKGKGYKPAETDTIGTWHGTGPYKINTGDFVKPKAAAPSWSGLVSGTVQRMAREDG
            RIVAITPAMPVGSKLEGFAKEFPDRMFDVGIAEQHAATMAAAMAQGMKPFLAIYSTF
            LQRAYDQVVHDICRNALSYDEGPIAMRFPRGNGLGVKMDEQLKTIGTWEVLRPGNDAVILT
            ENEGQHMVHTALSYDEGPIAMRFPRGNGLGVKMDEQLKTIGTWEVLRPGNDAVILT
            FGTTIEMAIEAEAELQKEGLSVRVVNARFIKPIDERKMKSILKEGLPILTIEEAVLEG
            GFGSSILEFAHDQGEYHTPIDRMGIPDRFIEHGSVTALLEEIGLTKQQVANRIRLLMP
            PKTHKGIGS"
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gene        complement(129877..130695)
            /gene="yqiD"
CDS         complement(129877..130695)
            /gene="yqiD"
            /function="unknown"
            /note="similar to geranyltransferase"
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            /codon_start=1
            /transl_table=11
            /protein_id="CAB14359.1"
            /db_xref="GI:2634862"
            /db_xref="SWISS-PROT:P54383"
            /translation="MTNKLTSFLADRKKTIENQLSVYTEKLDMPDSLKKSMLYSLQAG
            GKRLRPLIVLAVLNAYGKSEKDGIPVGCAVEMIHTYSLIHDDLPCMDDDDLRRGKPTN
            HKVFGEATAVLAGDLLTESFKLITSHVSDEVSAEKRLRIVNELISAAGTEGMVGGQV
            ADMEAGNRQVTLEELESIHERKTSKLLGFCVIAGAILADAPEEDIETLRTFSSHIGIG
            FQIRDDILDLEGSEEKIGKRVGSDTNDKSTYPSLSLLEGAKHKLDVHIKEAND"
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gene        complement(130685..130849)
            /gene="yqiC"
CDS         complement(130685..130849)
            /gene="yqiC"
            /function="unknown"
            /note="similar to exodeoxyribonuclease VII (small
            subunit)"
            /codon_start=1
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gene            complement(133902..134348)
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terminator      complement(133924..133924)
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CDS             complement(133941..134348)
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CDS             complement(134369..135721)
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                AIECRINAENPSKNFMPSPGEIKMYLPPGGLGVRVDSAAYPGYSIPPYDSMIAKVIT
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terminator      complement(136334..136352)
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                NYATEAIQTMTSFILALIPLLLALLASSGGAVSAAFFHPVIFLLMNTSGLLIQNIVMP
                LIFLSAILSIVSTMTEQYKVTQLANLLRNIAIGALAVFLTIFLGVISVQGASAAVTDG
                ITLRTAKFITGNFIPVLGRMFTDATDTVISASLLKNTVGLLGVALLICIAAFPAIKV
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                /gene="spoIIIAC"
gene            complement(139968..140174)
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                     /db_xref="SWISS-PROT:Q01367"
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                     EVMIVDEIGRMEDTDALLEALHAGVSVIVSAHGWSISDLMKRPSLKRLWEERAFDRYL
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CDS                   complement(147456. .147884)
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CDS                   153791. .155464
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CDS         156669. .157004
            /gene="sinR"
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terminator  156995. .157030
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            /note="alternate gene name: yqhD"
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CDS         complement(160154. .160528)
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gene        complement(160529. .160912)
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FLPFYRCEAEQLIERLKAGESIESAICGSLFYETDLSKVISHGQLSGRLDRELFTYSQ
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                     CNSPFFGFSPIKLFNSTLSLVPLVNPDGVDLVLNGSEVMGARRDELERLNEHRPNFN
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     gene            complement(172554..174506)
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     terminator      complement(172554..172582)
                     /gene="yqgS"
     CDS             complement(172590..174506)
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                     /function="unknown"
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                     /codon_start=1
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                     FINPLSFLLIFGLSLFLKGKNRNRYIIAMSCLVTFVLLANMVFYRFYNDFLTIPVLF
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                     ASVYFNLGLSEAERPQLLTRSFDREMLVKNISLFNFHIYDGVLQSKQSAQRALADSN
                     SLTEIENYVTANAKDANKRLFGAAKGRNVILVSLESTQSFVINEKLNGEEITPFLNDF
                     IKQSYNFNNVYHQTGQGKTSDSEFNVDNSLYPLGRGAVFFTNAGNQYMAAPELLKNSG
                     YYSAVLHANNKSFWNRDLMYDSFGYDSFFDINSYDVTDENTVGWGLKDKEFFEQSSEL
                     MKNLPQPFYSRLITLTNHFPFDLDEEDQLIDEYDSNSQTLNKYFPTVRYQDEALKRFI
                     EKLKEGLYDNSVIVLYGDHYGISENHNEAMGQFLGKEITPFEEVQLQKVPLVIHIPG
                     ITDKKPQTIETVGGQIDIRPTLMNLLGIDTKDQIQFGNDLLSDEKLDFTVLRDGSFIT
                     DQVVYTDGACYDKETGKPLEETKQCEAFADKAKQELSLSDEIIYGDLLRFYDQKRLDN
                     SSKRKEKQMLDQAS"

     gene            complement(174622..175587)
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     CDS             complement(174622..175587)
                     /gene="glcK"
                     /EC_number="2.7.1.2"
                     /note="alternate gene name: yqgR"
                     /codon_start=1
                     /transl_table=11
                     /product="glucose kinase"
                     /protein_id="CAB14416.1"
                     /db_xref="GI:2634919"
                     /db_xref="SWISS-PROT:P54495"
                     /translation="MDEIWFAGIDLGGTTIKLAFINQXGEIQHKWEVPTDKTGDTITV
                     TIAKTIDSKLDELQKPKHIIKYIGMGAPGPVDMAAGVVYETVNLGWKNYALKNHLETE
                     TGIPAVIENDANIAALGEMWKGAGDGAKDVILVTLGTGVGGIIANGEILHGINGAGG
                     EIGHICSIPEGGAPCNCGKTGCIETIASATGIVRIAKGKIANAKKTTRLKATEQLSAR
                     DVPEAAGENDEIALEVVDYVAKHLGLVLGNLASSLNPSKIVLGGGVSRAGELLRSKVE
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                     complement(175598..175813)

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CDS         /gene="yggQ"
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gene        /gene="yggP"
            complement(175923..177446)
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CDS         complement(175923..177446)
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            /note="similar to hypothetical proteins"
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            /translation="MFLLEYTYWKIAAHLVNSGVGVIQAGESDEIWLEAPDKSSHDLV
            RLYKHDLDFRQEMVRDIEEQAERVERVRHQLGRRRMKLLNVFFSTEAPVDDWEEIAKK
            TFEKGTVSVEPAIVRGTMLRDDLQAVFPSFRTEDCSEEHASFENAQMARERFLSLVLK
            QEEQRKTEAAVFQNGKPFTYLFIALQILMFSLLEINGGSTNTETLVAFGAKENSLIA
            QGEWRRLLTPIVLHIGIAHLAFNTLALWSGTAVERMYGSGRFLLIYLAAGITGSIAS
            FVFSPYPSAGASGAIFGCLGALLVALSNRKMFLRTIGTNIIVIIINLGFGFAVSNI
            DNSGHIGGLIGGFPAAAALGLPKAGAFGKRLLSAVFLIALAVGFSYYGLHSPSHQESA
            LIQQASELYQEGKYEEVTELLNGEAAQKDASADLKILAVSDIQIGEYDQAVSLLERA
            VKKEPKDHASYYNLALLYAEKNELAQAEKAIQTAVKLKPKEQRYKELQWQIENNKES"
gene        /gene="yggO"
            complement(177517..177709)
            /gene="yggO"
terminator  complement(177517..177533)
            /gene="yggO"
CDS         complement(177536..177709)
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            /function="unknown"
            /codon_start=1
            /transl_table=11
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            /db_xref="SWISS-PROT:P54492"
            /translation="MKKLLIYAIFAVSAVMFYQNRYRLMNTVDSQPGIRRSFIHLFLR
            IPFIRNKFIQQAF"
gene        /gene="yggN"
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            /gene="yggN"
CDS         complement(177776..178339)
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            /function="unknown"
            /note="similar to 5-formyltetrahydrofolate cyclo-ligase"
            /codon_start=1
            /transl_table=11
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            /db_xref="GI:2634923"
            /db_xref="SWISS-PROT:P54491"
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            PVIEKTKEVNPSQIDLMIVPGVCFDVNGFRVGFGGGYDRYLSEYEGKTVSLLLECQL
            FAHVPRLPHDIPVHKLLITEDRIISCFS"
gene        /gene="yggM"
            complement(178368..178394)
            /gene="yggM"
terminator  complement(178368..178394)
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CDS         complement(join(178368..178394,178657..179736))
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            /function="unknown"
            /note="similar to hypothetical proteins"
            /codon_start=1
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            /db_xref="SWISS-PROT:P54490"
            /translation="MNILMLSPEHPDEPKSGLGVHLNRLISYLNPHINITVFTPSGQL
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            GLESERKKVCREAPHYRLMTERLLIESADALIVLSTFMKRSLDKAAHKITVIPSPA
            SMEEEKGKIPRSMNRRFLFSYGRFVPEKGLSQLLKVFAILKQRQPDLYLVLAGEGPSL
            SCYEKLAAAYNLKDRIMFLPFLNRKDIRTLLSHCEMAVFPSSYEPFGLAAQESMEQGV
            LTVVSOSGFCDYAVHDKTAIIADFTLVQEAADLLDSFLKDREKARRIKEAGRQQVFK
            LHHPRLIMSSYLQLYERIFNNSAIH"
gene        /gene="yggL"
            complement(179733..180203)
CDS         complement(179733..180203)
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            /function="unknown"
            /codon_start=1
            /transl_table=11
            /protein_id="CAB14422.1"
            /db_xref="GI:2634925"
            /db_xref="SWISS-PROT:P54489"
            /translation="MDKHPFPYNIRHKLSFRDTFDIIIQNAHTLTVSWEISEETMRL
            AEAVLFEKTQDMIKELRIVIKRKDIEAVRTKRTTYDKGEWTIRQAAGDAVYRAEYRIV
            NSMNVSLKLAGTDDIYLDENGIRHINSFQIEEAHTRWEAQFSAYTCYGRGEKER"
gene        /gene="yqzD"
            180383..180736
CDS         180383..180736
            /gene="yqzD"
            /function="unknown"
            /codon_start=1
            /transl_table=11
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            /db_xref="GI:2634926"
            /db_xref="SPTREMBL:O32022"
            /translation="MEIAIALFIVSIALLIAFSYSQRDPMKDVEQELETLQLSAMOEI
            YKLKKKMTVLEEELLETNLVIRKSKONDINQKIAKOILSKYNNGMSAEAIAKAEHVSV
            EDVNTIIKDNEKVLV"
gene        /gene="yqzC"
            180733..181197
CDS         180733..181197
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            /function="unknown"
            /note="similar to hypothetical proteins from B. subtilis"
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            /transl_table=11
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            /db_xref="SPTREMBL:O32023"
            /translation="MTKRGIQAFAGGIILATAVLAAVFYLTDEDQAAAVKDNKTVTEQ
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            VSAILEKEGIISSAQDFNDYVIDAGYHKEIRAGKFPKVKSDMSFKKIVKTLTR"
gene        /gene="yggK"
            complement(181203..181219)
terminator  complement(181203..181219)
            /gene="yggK"
CDS         complement(181226..182008)
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            /function="unknown"
            /note="alternate gene name: yzmF
            similar to Phosphate ABC transporter (ATP-binding
            protein)"
            /codon_start=1
            /transl_table=11
            /protein_id="CAB14425.1"
            /db_xref="GI:2634928"
            /db_xref="SWISS-PROT:P46342"
            /translation="MSIATEAVMKQEVYQVGMNLWYGQHHALKNINLSIYENEVTAI
            IGPSGCGKSTFIKTLNLMIQMTPNVKLAGELNYNGSNILKDKVDIVDLRKNIGMVFQK
            GNPFPQSIFDNVAYGPRVHGTKNKKLQEVEKSLKDVALMDEVKDRLHTSALSLSGG
            QQQRLCIARALATNPDILLMDEPTSALDPISTRKIEELILELKDKYTIVTHNMQQA
            ARVSDQTAFFYMGELVECDNTNKMFSNPKDQRTLDYISGKFG"
gene        /gene="yggJ"
            complement(182019..182828)
CDS         complement(182019..182828)
            /gene="yggJ"
            /function="unknown"
            /note="alternate gene name: yzmE
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                    similar to phosphate ABC transporter (ATP-binding
                    protein)"
                    /codon_start=1
                    /transl_table=11
                    /protein_id="CAB14426.1"
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                    /db_xref="SWISS-PROT:P46341"
                    /translation="MSEQMVKEKPERAVIVPKQNHVLEVKDLSIYYGNKQAVHHVNMD
                    IEKNAVTALIGPSGCGKSTFLRNINRMNDLIPSARAEGEILYEGLNILGGNINVVSLR
                    REIGMVFQKPNPFPKSIYANTHALLYAGERNKAVLDEIVEESLTKAALMDEVKDRLH
                    SSALSLSGGQQRLCIARTLAMKPAVLLDEPASALDPISNAKIEELITGLKREYSII
                    IVTHNMQQALRVSDRTAFFLNGELVEYGCQTEQIFTSPKKQKTEDYINGKFG"
gene                complement(182849. .183733)
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CDS                 complement(182849. .183733)
                    /gene="yqgI"
                    /function="unknown"
                    /note="alternate gene name: yzmD
                    similar to phosphate ABC transporter (permease)"
                    /codon_start=1
                    /transl_table=11
                    /protein_id="CAB14427.1"
                    /db_xref="GI:2634930"
                    /db_xref="SWISS-PROT:P46340"
                    /translation="MNRKITDKLATGMFGLCAAIIAAILVGLFSYIIINGVSQLSFQF
                    ITTKSSAIAGGGCIRDQLFNSFYILFITMLITIPLGVGGGVFMAEYAPNNKVTDFIRT
                    CIEVLSSLPSIVIGMFGLLMFVNLTGWGYTIIGGALALTVFNLPVMVRVTEDAIRSVP
                    KDLKEASLALGVSRWHTVKTVLIPSAIPSIITGAILASGRVFGEAAALLFTAGLTTPR
                    LNFTEWNPFSETSPLNIFRPAETLAVHIWNVNTQGMIPDAEAIANGGSPVLVISVLVF
                    NLAARWLGTMIYKKLTAN"
gene                complement(183733. .184662)
                    /gene="yqgH"
CDS                 complement(183733. .184662)
                    /gene="yqgH"
                    /function="unknown"
                    /note="alternate gene name: yzmC
                    similar to phosphate ABC transporter (permease)"
                    /codon_start=1
                    /transl_table=11
                    /protein_id="CAB14428.1"
                    /db_xref="GI:2634931"
                    /db_xref="SWISS-PROT:P46339"
                    /translation="MINNRENMSVSERLISSRQNRQLDEVRGRMIVTACALIMIAASV
                    AITIFLGVKGLQSFLVNGVSPIEFLTSLNWNPTDSDPKYGVLPFIFGSFAVTILSALI
                    AAPLGIAGPIFMTEIAPNWGKKVLQPVIELLVGIPSVVVGFIGLTVLVPFIAQFKSSG
                    TGHSLLAGTIVLSVMILPTITSISADAMASLPKSLREGSYALGATRWQTIRKVLVPAA
                    FPTLMTAVVLGMARAFGEALAVQMVIGNTRVLPESPFDTAGTLTTIITLNMGHTYGS
                    VENNTLWSMGLVLLVMSFLFILLIRYLSSRRKV"
gene                complement(184731. .185633)
                    /gene="yqgG"
CDS                 complement(184731. .185633)
                    /gene="yqgG"
                    /function="unknown"
                    /note="alternate gene name: yzmB
                    similar to phosphate ABC transporter (binding protein)"
                    /codon_start=1
                    /transl_table=11
                    /protein_id="CAB14429.1"
                    /db_xref="GI:2634932"
                    /db_xref="SWISS-PROT:P46338"
                    /translation="MKKNKLVLMLLMAAFMMIAAACGNAGESKKSNSDSAKGEEKASG
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                    EEKEGIDAKALVDHQVAVVGMAAAVNPDAGVKDISKDELKKIFTGKIKNWKELGGKDQ
                    KITLVNRPDSSGTRATFVKYALDGAEPAEGITEDSSNTVKKIIADTPGAIGYLAFSYL
                    TDDKVTALSIDGVKPEAKNVATGEYPIWAYQHSVTKGEATGLAKEFLDYLKSEDIQKS
                    IVTDQGYIPVTDMKVTRDANGKQS"
gene                complement(185762. .187937)
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terminator          complement(185762. .185780)
                    /gene="pbpA"
CDS                 complement(185787. .187937)
                    /gene="pbpA"
                    /function="involved in the synthesis of peptidoglycan
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                    associated with cell wall elongation in spore outgrowth
                    (peptidoglycan biosynthesis)"
                    /note="alternate gene name: yqgF
                    /codon_start=1
                    /transl_table=11
                    /product="penicillin-binding protein 2A"
                    /protein_id="CAB14430.1"
                    /db_xref="GI:2634933"
                    /db_xref="SWISS-PROT:P54488"
                    /translation="MRRNKPKQNHKEKKSLPIRLNILFLAAFVIFTWIIVELGIKQ
                    IVQGDDYKNQANKQEQSEVSSAVPRGKIYDRNFNAIYTNKALNAITYTRSKSTTQEQR
                    LKIAKKLSDMIKVDTKKVTERDKKDWILTRPKEAKKLISSKERQQVEDKKISDDDLY
                    QLQLKRITDKQLNELTDKMQIAIKRQMDSGYALTPQYIKNEDVSAKEMAVVSEHLD
                    ELPGVDTSDWEREYPYKNLLRSVLGSVSSNEGLPSNLLDHYLSLGYSRNDRVGKSY
                    LEYQYESLLQGQKAKVENITDSKGNVTGTKTVSEGKAGKDLVLTIDIDLQKSVEKIIE
                    KKLKAAKARPSTELLDRAFVVMDPRNGEVLTMAGKQIKRENGAYKFDDYALGAMTSS
                    YAMGSAVKGATVLTGLQTGAINLNTVFKDEPLYIGQDKRGKKSWQNLGPVGIQTALEK
                    SSNVFMKTAIAVGKGEYKPHQALPLDTSAFDTFRNYFSQFGLGVKTGIDLPNEMTGY
                    KGTSRLSGFLLDFAIGQYDTYTPLELAQYVSTIANGGYRMKPQLVKEVRDSNAKKGIG
                    AVVDSVQPEVLNKVDMKSSYIEEVQAGFRRVATKGTAAGQLASASYKPAAKTGTAQSF
                    YDGPDKSKTGTDYTNTTLVAYAPADNPEIAISVVVPWTYIDYNQRYSITNEIGREVMD
                    KYFELKSKQDKEGTQQKNKDKIEENAENTTSSDN"
gene                complement(188051. .189343)
                    /gene="yqgE"
CDS                 complement(188051. .189343)
                    /gene="yqgE"
                    /function="unknown"
                    /note="similar to hypothetical proteins"
                    /codon_start=1
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                    /db_xref="GI:2634934"
                    /db_xref="SWISS-PROT:P54487"
                    /translation="MSKIKKVIGDVDVNKGLLFLLTIGGLYSLGIALSNTFVNVYLWK
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                    AGFVISRLENNTGYTVIFSLSLSLLAVVMSFRMLSKVFGGSRGFMLSKVFGERHSNMN
                    WRRITNAHFFQGLREGIFVFLISVFVFIETNSELALGTFGLVNSAVSPLAYYFASRLI
                    KKKARKKSILLGGLILYGALFLILFHMSFSTLLTYGVFIAIGYPLLLVPYVSLTYDVI
                    GRARHARKARIEYIVLREMFLNAGRIVSILCFLLIVALLKEDVGIPLSLAILGIGHPL
                    IYYFVKDIRFKEKEGENETMEEDGQKRVTEPTLLKGER"
gene                complement(189377. .190057)
                    /gene="sodA"
CDS                 complement(189377. .190057)
                    /gene="sodA"
                    /EC_number="1.15.1.1"
                    /note="alternate gene name: yqgD"
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                    /product="superoxide dismutase"
                    /protein_id="CAB14432.1"
                    /db_xref="GI:2634935"
                    /db_xref="SWISS-PROT:P54375"
                    /translation="MAYELPELPYAYDALEPHIDKETMTIHHTKHHNTYVTNLNKAVE
                    GNTALANKSVEELVADLDSVPENIRTAVRNGGGHANHKLFWTLLSPNGGGEPTGALA
                    EEINSVPGSFDKFKEQFAAAAGRFGSGWAWLVVNGKLEITSTPNQDSPLSEGKTPI
                    LGLDVWEHAYLNYQNRRPDYISAFWNVVNWDEVARLYSDENNGTNKVLIMGPCFFMS
                    SFYISRFE"
gene                complement(190236. .190718)
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CDS                 complement(190236. .190718)
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                    /function="unknown"
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                    /transl_table=11
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                    /db_xref="SWISS-PROT:P54486"
                    /translation="MDMLYWLLIAAVFIIAFIGLVPVIPSVFIVAGFVLYGFLFSF
                    SPYSYMFWLVEAVFAAVLFAADVSNLLGVKRFGGSKAAIWGSTIGLLIGPFVIVAG
                    IILGPFIGAVCAELIVHQKDLKSAFKIGLGSLIGFLTGVIAKGIIQLLMIGFLWTVL"
gene                190828. .191586
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CDS
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190828..191586
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/function="unknown"
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/db_xref="SWISS-PROT:P54485"
/translation="MNVFQLFIKSTYSPRDIAKTRFQGIGKAILYVFLLSVLFAIPTA
YVVSTGTVKSMNGFKTVLNKDFPDFTISNGKLQTDEKKATESQANGFVIVFDPTDSYG
TEQIEAKQNAIGILQNKFVLAIDGQAQEMSYSMMPSELQKKDVIAGLNQNKAMIVTVL
SALIFLVTAAGKFIEVSFLALIGLIIKNSOKKHLSYHQLWKLSAYSITLSTVFFTIMR
ALEATVPSEFLLNWFVNFVILFLVLKEIPVQKSN"
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gene
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/gene="yggA"
complement(191922..192440)
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terminator
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complement(191922..191946)
/gene="yggA"
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CDS
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complement(192012..192440)
/gene="yggA"
/function="unknown"
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/db_xref="SWISS-PROT:P54484"
/translation="MKQGKFSVFLILLMLTLVVAPKGKAEAASSGWQPVSGISGCKI
RVITDAYTYTKSATSIDAYAETNGKCGKLNYKSFGVSIVEGGDIGPQYSGYFSSRTPT
KKFYFSKLPKPTGIPWAVGLSVYKGKAKGAAFVYINPQKR"
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gene
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/gene="yqfZ"
192717..193016
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CDS
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192717..193016
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/protein_id="CAB14436.1"
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/db_xref="SWISS-PROT:P54483"
/translation="MKRLTLVCSIVFILFILFYDLKIGTIPIQDLPVYEASAKTAVQE
PAYKTVKVKPGDFVMSIVGSAGSPDDIVKDFEALNPNVKANAIQAGTAYKFPVYP"
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gene
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/gene="yqfY"
193139..194272
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CDS
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193139..194272
/gene="yqfY"
/function="unknown"
/note="similar to peptidoglycan acetylation"
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/transl_table=11
/protein_id="CAB14437.1"
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/db_xref="SWISS-PROT:P54482"
/translation="MQVSEITHRTKTRPVKVGPLTIGGNNEVVIQSMTTKTHDVEAT
VAEINRLAEAGCQIVRVACPDERAANAIADIKKRISIPLVVDIHFDYKLALKAIEGGA
DKIRINPGNIGRREKVEAVVKAAKDKGIPIRIGVNAGSLEKRILEKYGPTADGMVES
ALHHIKILEDLDFHDIIVSMKASDVNLAIEAYEKAAKAFDYPLHLGITESGTLFAGTV
KSAAGLGAILSKGIGNTMRISLSADPVEEVKVARELLKSFGLASNAATLISCPTCGRI
EIDLISIANEVEEYISKIKAPIKVAVLGCAVNGPGEAREADIGLAGARGEGLLFRKGK
IVRKVPEETMVEELKKEIDILAEEHYAKLEAEKALKEETQKA"
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gene
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complement(join(194267..194288,194298..194687))
/gene="yqfX"
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terminator
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complement(194267..194288)
/gene="yqfX"
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CDS
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complement(194298..194687)
/gene="yqfX"
/function="unknown"
/codon_start=1
/transl_table=11
/protein_id="CAB14438.1"
/db_xref="GI:2634941"
/db_xref="SWISS-PROT:P54481"
/translation="MKVANDYEKRDNNSYYVDHGSEGTNITRDNDGFFEETAAEIAEP
YRAADRSNDQDNDRSGGNVNEGRGIYIALALSIISLFVLPVLLGAAGIVGYIARR
GAQGLGAWAMGIGVVSLVLGIFIIPFF"
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gene
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/gene="yqfW"
194820..195401
/gene="yqfW"
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CDS
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194820..195401
/gene="yqfW"
/function="unknown"
/codon_start=1
/transl_table=11
/protein_id="CAB14439.1"
/db_xref="GI:2634942"
/db_xref="SWISS-PROT:P54480"
/translation="MLRLGIDIGTITAQDTFVPYLNRSFNLSISLNDMTDYDLTKLL
NITQEFWDWMNQNEAIIYKEALLAQHAKQSLDLLKEEHKLIYITARRTHLTDITYEW
FDRQNIHYDHIELVGGHHKVEAVKNHNIDLFFEDHHGNAMMIAKEAGIPVILFNSPYN
QLPIDSNIIRVNNWLEAVQWMNNNKHHLIRVNN"
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gene
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/gene="yqfV"
complement(195406..195881)
/gene="yqfV"
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terminator
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complement(195406..195424)
/gene="yqfV"
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CDS
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complement(195444..195881)
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terminator
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GEFVMFINVFIFIWAVFVFGGPEQAMYSFMTYYIAMKTIDAVIQGLDETKAVIVSEQY
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gene
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197016..197292
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197016..197270
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terminator
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197275..197292
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gene
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complement(197297..198190)
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CDS
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                      /db_xref="SWISS-PROT:P54475"
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CDS                   199685..200428
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                      /db_xref="SWISS-PROT:P54474"
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                      LKTSAPKKKEAASPAPKRTSGSSKPRLYI"
gene                  200551..201512
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CDS                   200551..201495
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                      SEKLIVTNQTTMSQWDVHDIMELVKEKYPHVEYHQEICLATQVRQEAVSEQAKKADLT
                      IVVGDPKSNNSNRLAQVSEEIAGTKAYRIGDLSELKLEWLKGVNTVAVTAGASTPTPI
                      TKEVIRFLEQFQDHEDPSTWTTEHNIPLKKILPKVKAKN"
terminator            201492..201512
gene                  complement(201518..202639)
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CDS                   complement(201518..202639)
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                      /note="similar to hypothetical proteins"
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                      AGHIGEYSHCAFSSEGITGSFKPLDRGAHFSVSMSGKHMLLAASQEAVSYGANTRRK
                      AMIKSHPYEEVAYDIYPVEQTPAEKGLGRVGTLKNEMTLKEFALFVKDLDVNGVRMV
                      GDADSMVKKVAVLGGDGNKYIHHAKRKGADVVTGDLYFHVAHDAMMLGLNVVDPGHY
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gene                  complement(202632..203282)
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CDS                   complement(202632..203282)
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                      /db_xref="SWISS-PROT:P54471"
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gene                  complement(203401..203901)
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terminator            complement(203401..203421)
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CDS                   complement(203539..203901)
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                      /db_xref="SWISS-PROT:P24469"
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gene                  complement(204202..205345)
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CDS                   complement(204230..205345)
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                      /protein_id="CAB14450.1"
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                      LDLIHEGNMGLMKAVEKFDYRKGYKFSTYATWWIRQAITRAIADQARTIRIPVHMVET
                      INKLIRVQRQLIQDLGREPTPEEIAEDMDLTPEKVREILKIAQEPVSLETPIGEEDDS
                      HLGDFIEDQEATSPSDHAAYELLKEQLEDVLDTDREENVLRFGLDDGRTRTLEE
                      VGKVFGVTRERIRQIEAKALRKLRHPSRSKRLKDFLE"
gene                  complement(205544..207355)
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CDS                   complement(205544..207355)
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                      /function="initiation of Okazaki fragments (DNA
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                      /note="alternate gene name: dnaE"
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                      /transl_table=11
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                      /db_xref="SWISS-PROT:P05096"
                      /translation="MGNRIPDEIVDQVQKSADIVEVIGDYVOLKKQRNYFGLCPFHG
                      ESTPSFSVSPDKQIFHCFGCGAGGNVFSFLRQMEGYSFAESVSHLADKYQIDFPDDIT
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                SQYLAHKRLKVANVPIVPEVDPPEELFNVDPKKCIGLKISPDKLNHIRKERLKSLGLN
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                RKOMIOSQLETMAAENNWSIPVDEDLLDEVNHLVEYPTALYGSPESEFLSIPPEVLVT
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                QKLNIDANVKKLENIVFHEELGSLADKVRRVTSIAEKLAVRLQADEDTLKHVKRAAEI"

                SKFDLVTHMIYEFPELQGIMGEKYARMLGEDEAVAAAVNEHYMPRSAGGETPSTFGA
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                TDKENELLDFFTQRLKYVLNAEQIRHDVIDAVLESSELEPYSALHKAQVLEQKLGAPG
                FKETAEALGRVISIKKGVRGDIQPDLFENEYEAKLFDAYQTAKENLQENFSKKKDYEA
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                PLEHDIRFVEDNWENFSLSGCAGLGWEVWLDGMEITQFTYFQQVGGLECKPVSVEITYG
                IERLASYIQDKEHVFDLEWTSGFTVKDLPMEAEYEHSVYTFETSDVDMLQFLFSTYEK
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                IETLLAQIEAYLPEGPQFYPSDQVTDHPERFIISELIREKVLHLTREEIPHSIAVAIE
                SIKGQDNGSVHVAAFIVVERDSQKGIVIGKKGSLLKEVGKRARADIEALLGSRVYLEL
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                /protein_id="CAB14459.1"
                /db_xref="GI:2634962"
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CDS           complement(215472..215816)
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              /EC_number="2.7.1.107"
              /function="phospholipid biosynthesis"
              /note="alternate gene name: yqxF"
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              /transl_table=11
              /product="diacylglycerol kinase"
              /protein_id="CAB14460.1"
              /db_xref="GI:2634963"
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              SIIEWMIIFLLIGGMFSLELLNTAIEHTVDLITDKHHPLAKAAKDAAAGAVCVFAVIS
              CIIGLLIFLPKL"
gene          complement(215823..216296)
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CDS           complement(215823..216296)
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              /note="similar to hypothetical proteins"
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              /translation="MSLLIDIVDETGSVSEEMLKEVENLLQFAAREGVQDQAEVSVT
              IVSNDDIHQINKEYRGKDAPFDVISFALEEEGEGEIEIVGAEMPPVLGNIIISADRTR
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gene          complement(216297..218432)
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CDS           complement(216297..218432)
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BASE COUNT    58190 a    51645 c   43161 g   65474 t
ORIGIN
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CCGACAATTAATACGTCGCAAATC--TCTTTTCATTT--GCCTTCAATGCGGCTAACGATGGATCTGC
131010      131020       131030       131040       131050       131060       131070

              170         180         190         200         210         220         230
              -CGCAGTTACCGACGAGGCCGGGGCAGCACGCTGAAGGACTTTATCCCCGTACAGGGAGTCTACGCAGCG
TCGCATTTT--CACCTTGTACGGAGCCGCCGGGAAGAACAATGCAGTTT--TACAAGGGGATATCTTCTTTTTAGAG
131080      131090       131100       131110       131120       131130       131140

              240         250         260         270         280         290
              -GGACGCTCGGATCGC-GACAGCGAGGGGGTGCTCGGTCCT-TACCAATGACG-GCGT-GCT--CCAGGCCAG
TTGTAATAACG-TCTCTGACACGCG-GCACCCGTTGGAGATGTCACACCCCGATTGTGGCGTGGAAATGCGGG
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TAAAT---AAAGCGGCTCCAACCCCGTCAGGCGCATTCTTTGGCA-TATAATGAAGTTTCCGCTCG-GT
31280      131290       131300       131310       131320       131330       131340

              440         450         460         470         480         490         500
GAATGAACCCGAGT---GGCTGTGGCC-GCGC-AACCCGCCGATTCGTGAGCGT--AAATCCATTCCTACCA
TCATATACGGAAATTCCGCCCTCGACCAGCACTTTCATTCCGTTT--TCAGGTTTAAAGGCAGAGCGCTCGC
131350      131360       131370       131380       131390       131400       131410

              510         520         530         540         550         560
GCTGGCT---TAAAATCACC--CTTTATGAAGGCCGCAACCGACAGGTCAGGCG-CATGACT--GC--GCAT
TTTGTCTCGGCAGACATCACCAGCGCAT-TCTGCCCTTTTCGCTTCTTTAAGTGAAATAAAATATGCCCTCGT
131420      131430       131440       131450       131460       131470       131480

              570         580         590         600         610         620         630
GTGGGCTTCCTACCCTGCGACTCATTCGC---TACGCCATGGGCAGCTATACGGTGGACTCGCGTGGCAAAC
GTGTGTATCTTTA-CATTCGAC-AATTCGGCCTTTAATCCA--AATATTTCAAGGT-GAGAGTCT-----AC
131490      131500       131510       131520       131530       131540

              640         650         660
GGGAATGGCGGGATGTTACCCCTAAGGAGAACTGA                    x
ATCGGAATTTCGTTTTATATACTTTGTCAGCGTCGAGACGGTCACATACGCTGCTTCACCCATGTCTAAAA
31550      131560       131570       131580       131590       131600       131610       131620

CTCCTCCTCAAGC
131630
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4.  US-09-252-691C-1394 (1-669)
    ae000213        TOIG of:,ae000213    check: 1875    from: 1    to: 10959

    TOIG of: ae000213    check: 1875   from: 1    to: 10959

LOCUS       AE000213    10959 bp    DNA              BCT        01-DEC-2000
DEFINITION  Escherichia coli K12 MG1655 section 103 of 400 of the complete
            genome.
ACCESSION   AE000213 U00096
VERSION     AE000213.1  GI:1787371
KEYWORDS    .
SOURCE      Escherichia coli K12
ORGANISM    Escherichia coli K12
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
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Z99116 Length: 218470  September 24, 2001 09:21  Type: N  Check: 4068  ..

Initial Score      =  52    Optimized Score       =    288    Significance  =   0.09
Residue Identity   =  48%   Matches               =    341    Mismatches    =   293
Gaps               =  72    Conservative Substitutions =            0
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         30           40           50           60           70           80          90
ACGCCTGAAAATACCATG-ACGAAAACTTCTT-TTAGAAAAACCACCGGGTTGAGCGATTCAGCTCACGACAAG
|-|||||| || |||||||||| ||||| ||||  ||||||| |||||||||||| |||| |||||||||||||
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REFERENCE   1  (bases 1 to 10959)
  AUTHORS   Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau.B. and Shao,Y.
  TITLE     The complete genome sequence of Escherichia coli K-12
  JOURNAL   Science 277 (5331), 1453-1474 (1997)
  MEDLINE   97426617
   PUBMED   9278503
REFERENCE   2  (bases 1 to 10959)
  AUTHORS   Blattner,F.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   3  (bases 1 to 10959)
  AUTHORS   Blattner,F.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   4  (bases 1 to 10959)
  AUTHORS   Plunkett,G. III.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-1998) Laboratory of Genetics, University of
            Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
  COMMENT   This sequence was determined by the E. coli Genome Project at the
            University of Wisconsin-Madison (Frederick R. Blattner, director).
            Supported by NIH grants HG00301 and HG01428 (from the Human Genome
            Project and NCHGR). The entire sequence was independently
            determined from E. coli K12 strain MG1655. Predicted open reading
            frames were determined using GeneMark software, kindly supplied by
            Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
            30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that
            have been correlated with genetic loci are being annotated with CG
            Site Nos. unique ID nos. for the genes in the E. coli Genetic
            Stock Center (CGSC) database at Yale University, kindly supplied by
            Mary Berlyn. A public version of the database is accessible
            (http://cgsc.biology.yale.edu). Annotation of the genome is an
            ongoing task whose goal is to make the genome sequence more useful
            by correlating it with other data.  Comments to the authors are
            appreciated. Updated information will be available at the E. coli
            Genome Project's World Wide Web site
            (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and
            its annotations are periodically updated; this is version M54. No
            sequence changes. Annotation updates: updated gene identifications
            and products; all new functional assignments courtesy of Monica
            Riley; added promoters, protein binding sites, and repeated
            sequences described in reference 1. The unique numeric identifiers
            beginning with a lowercase 'b' assigned to each gene (protein- or
            RNA-encoding) are now designated as gene synonyms instead of
            labels. This should allow them to be searched for in Entrez as gene
            names.
FEATURES             Location/Qualifiers
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                     PHGDIRVAFTPDEEVGKGAKHFDVDAFDARWAYTVDGGVGCELEFENFNAASVNIKIV
                     GNNVHPGTAKGVMVNALSLAARIHAEVPADESPEWTEGYEGFYHLASMKGTVERADMH
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BASE COUNT   2685 a   2752 c   2819 g   2703 t

ORIGIN

AE000213 Length: 10959 September 24, 2001 09:14 Type: N Check: 1875 ..

Initial Score   =   35   Optimized Score   =   288   Significance   = -0.65
Residue Identity =   49%   Matches   =   360   Mismatches   =   267
Gaps   =   103   Conservative Substitutions   0

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SOURCE   Escherichia coli K12.
ORGANISM   Escherichia coli K12
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1 (bases 1 to 11961)
AUTHORS   Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau,B. and Shao,Y.
TITLE   The complete genome sequence of Escherichia coli K-12
JOURNAL   Science 277 (5331), 1453-1474 (1997)
MEDLINE   97426617
PUBMED   9278503
REFERENCE   2 (bases 1 to 11961)
AUTHORS   Blattner,F.R.
TITLE   Direct Submission
JOURNAL   Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   3 (bases 1 to 11961)
AUTHORS   Blattner,F.R.
TITLE   Direct Submission
JOURNAL   Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   4 (bases 1 to 11961)
AUTHORS   Plunkett,G. III.
TITLE   Direct Submission
JOURNAL   Submitted (13-OCT-1998) Laboratory of Genetics, University of
            Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
COMMENT   This sequence was determined by the E. coli Genome Project at the
            University of Wisconsin-Madison (Frederick R. Blattner, director).
            Supported by NIH grants HG00301 and HG01428 (from the Human Genome
            Project and NCHGR). The entire sequence was independently
            determined from E. coli K12 strain MG1655. Predicted open reading
            frames were determined using GeneMark software, kindly supplied by
            Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
            30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that
            have been correlated with genetic loci are being annotated with CG
            Site Nos., unique ID nos. for the genes in the E. coli Genetic
            Stock Center (CGSC) database at Yale University, kindly supplied by
            Mary Berlyn. A public version of the database is accessible
            (http://cgsc.biology.yale.edu). Annotation of the genome is an
            ongoing task whose goal is to make the genome sequence more useful
            by correlating it with other data. Comments to the authors are
            appreciated. Updated information will be available at the E. coli
            Genome Project's World Wide Web site
            (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and
            its annotation are periodically updated; this is version M54. No
            sequence changes. Annotation updates: updated gene identifications
            and products; all new functional assignments courtesy of Monica
            Riley; added promoters, protein binding sites, and repeated
            sequences described in reference 1. The unique numeric identifiers
            beginning with a lowercase 'b' assigned to each gene (protein- or
            RNA-encoding) are now designated as gene synonyms instead of gene
            labels. This should allow them to be searched for in Entrez as gene
            names.
FEATURES   Location/Qualifiers
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     CAAGCC-ACCAG-AAGAACGCCAGAACCCCAGCCAA---  -CGCGGG--TCATAC----TGTT--CAATAAAC
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2950              2960      2970      2980      2990      3000
          220       230       240       250       260       270       280
     GAGTCTCACGCAGCGCGGGACGTCTGGATC-GCGACAGCGAGGGGCTCCTGGGTCCTTACCAATGACGGCGTGCTC
     ||  ||        |||  | |||      |  | | ||  || || ||   ||      |  ||||  | | |   |
     ACCCCTTGCGTTGATACACTTTGTTCAGCG-CTG--AGGTG-AGATTGTCC--AGCAGTG-GGGCG-ACCG
3010             3020       3030      3040      3050      3060      3070
          290       300       310       320       330       340       350
     CAGGCCAGGCTACTCAGCCGGGCAA--ACGTACCGGAAAAATTTACTACTGTCAGGTTGAAGGCGA--GC
     | | ||   | |    |  |||||||  || ||| |     |||| |     |||| |||   |     ||
     GATGC-AG-CT--CGCGGCGTGAGCAATGTCCCGCGCCGGCATAACTGCCACGATGCAGGTAGTAGCCAATTTGC
3080             3090       3100      3110      3120      3130      3140
          360       370       380       390       400       410
     CGGAGCACGCGCTCGCGTGGCAAAGCTGT-GCA--AC-GGC---GTAACGCTGAACG---ACGGTCCCACCCTG
     |||  |  |     |  |   || ||| |  | ||  | | |  |    || ||      ||||  |||||| |||
     TGTGAAATGCG--GCT-GATTTGCTCCAGCATTACCGGCTCAGCATCACTG-ACGCTCATCTTTTCACTACG
3150             3160       3170      3180      3190      3200
          420       430       440       450       460       470       480
     CCG-GCTGGTATTGAAACGTGTGAAATGAACCCGAGTGGTGCTGTGGCCCGCGCAACCCGCGATTCGTCGAGCGT--
     | |  |    |  ||||| | | | |  | |      ||  |  ||| |||||  | |  |||| |  |  |||||||
     CAGAGAACGCAGGCGTAC-TTTGCAGCACCCCAGTGGCGTTTCAGACTATGGGCGTCAGGTCGGTCGGTGAGCGGTCG
3210             3220       3230      3240      3250      3260      3270
          490       500       510       520       530       540
     AAATCCATT---CCTACCAGCTGGC-TTAA---AATCACCCTTTATGAAGG--CCGCAACGCAGCAGGTCAG-
     |||  ||         |      ||| |  ||  | | |  |  | | |  |     | |||  | | |||| |||||
     TACGGTATTTGTCGGTAAC-GTTCGGCGTCACTGTTTTAACAATCGGTTTCGTACCAGACTGGTCAGT
3280             3290       3300      3310      3320      3330      3340      3350
          550       560       570       580       590       600       610
     --GCGCATGACTGC-GCATGTGGGC--TTCCCTACCCTGCGACTCATTCGGCTACGGCCATGGCCAGTATACG
     ||        |    |   | ||    |    | | |    |  |      ||     |   |  ||  |||||
     TCTCCGCTTGTGGCTGGAT-TGAGCAATTGCGGGTTATG---TTCTTCCAGTTCGC----GGACTTCTTTTGC
3360             3370       3380      3390      3400      3410
          620       630       640       650       660
     CTGGAC-TCCCTG---GCAAACGGGGAATGGCGG-GATGTTACCCCTAAGGAACTGA          X
     | ||| |  |||||       ||  ||  |     || ||      |  |  | ||||  |||  ||
     CAGGGCTTCGATGGGCGTAAACTCCACCAGCGGCGACCCACAGCCGGATCAACAGCAGATTGGC
3420             3430       3440      3450      3460      3470    X 3480
     TGAGAGCACATAGATAAAACCAGCTCCAGACCATATAGG
3490             3500       3510      3520
```

5. US-09-252-691C-1394 (1-669)
     ae000308   TOIG of: ae000308   check: 6916   from: 1   to: 11961

     TOIG of: ae000308   check: 6916   from: 1   to: 11961

LOCUS   AE000308   11961 bp   DNA   BCT   01-DEC-2000
DEFINITION Escherichia coli K12 MG1655 section 198 of 400 of the complete
            genome.
ACCESSION   AE000308 U00096
VERSION   AE000308.1 GI:1788508
KEYWORDS   .

CDS
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                /note="f396; 99 pct identical to BCR_ECOLI SW: P28246"
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                /transl_table=11
                /product="bicyclomycin resistance protein; transmembrane
                protein"
                /protein_id="AAC75243.1"
                /db_xref="GI:1788509"
                /translation="MTTRQHSSFAIVFIIGLLAMLMPLSIDMYLPALPVISAQFGVPA
                GSTQMTLSTYILGFALGQLIYGPMADSFGRKPVVLGGTLVFAAAVACALANTIDQLI
                VMRRFHGLAAAAASVINALMRDIYPKEESFRMMSFVMLVTTIAPLMAPIVGGWVLVW
                LSWHYIFWILALAILASAMIFFLIKETLPPERRQPFHIRTTIGNFAALFRHKRVLSY
                MLASGFSFAGMFSFLSAGPFVYIEINHVAPENFGYYFALNIVFLFVMTISRSFVRRI
                GALNMFRSGLWIQFIMAAWMVISALLGLGFWSLLVGVAAFVGCVSMVSSNAMAVILDE
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                PKKR"
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gene
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                complement(1415..2110)
                /gene="rsuA"
                /note="b2183"
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CDS
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                /function="enzyme; RNA synthesis, modification, DNA
                transcription"
                /note="f231; formerly designated yejD"
                /codon_start=1
                /transl_table=11
                /product="16S pseudouridylate 516 synthase"
                /protein_id="AAC75244.1"
                /db_xref="GI:1788510"
                /translation="MRLDKFIAQQLGVSRAIAGREIRGNRVTVDGEIVRNAAFKLLPE
                HDVAYDGNPLAQQHGPRYFMLNKPQGYVCSTGDPDHPTVLYFLDEPVAWKLHAAGRLD
                IDTGLVLMTDDGQWSHRITSPRHHCEKTYLVTLESPVADDTAEQFAKGVQLHNEKDL
                TKPAVLEVITPTQVRLTISEGRYHQVKRMFAAVGNHVVELHRERIGGITLDADDLAPGE
                YRPLTEEIASVV"
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                complement(1451..1479)
                /gene="rsuA"
                /note="factor Sigma70; predicted +1 start at 2277837"
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protein_bind
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                complement(1626..1650)
                /gene="rsuA"
                /note="central position to predicted promoter: -170.5"
                /bound_moiety="CynR predicted site"
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promoter
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                2167..2197
                /note="factor Sigma70; predicted +1 start at 2278597"
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gene
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                2259..4019
                /gene="yejH"
                /note="b2184"
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CDS
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                /gene="yejH"
                /function="putative enzyme; Not classified"
                /note="o586; residues 1-396 are 100 pct identical to 396
                residues of YEJH_ECOLI SW: P33919 (403 aa) and residues
                493-586 are 100 pct identical to aa 2-95 of YEJI_ECOLI SW:
                P36927; residues 404-477 are 100 pct identical to
                YEJI_ECOLI SW: P36926 (89aa)"
                /codon_start=1
                /transl_table=11
                /product="putative ATP-dependent helicase"
                /protein_id="AAC75245.1"
                /db_xref="GI:1788511"
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                IYQFPYHGMVRGDEKALFRDCIYELPLRYMIKHGYLTPPERLDMPVVQYDFSRLQAQS
                NGLFSEADLNRELKKQQRITPHIISQIMEFAATRKGVMIFAATVEHAKEIVGLLPAED
                AALITGDTPGAERDVLIENFKAQRFRYLVNVAVLTTGFDAPHVDLIAILRPTESVSLY
                QQIVGRGLRLAPGKTDCLILDYAGNPHDLYAPEVGTPKGKSDNVPVQVFCPACGFANT
                FWGKTTADGTLIEHFGRRCQGWFEDDDGHREQCDFRFRRKNCPQCNAENDIAARCRE
                CDTVVDPDDLMKRLKAALRLDKALVLRCSGMSLQHGHDEKGEWLKITYDEDGADVSWEF
                RLQTPAQRTAFEQLFIRPHTRTPGIPLRWITAADILAQQALLRHPDFVVARMKGQYWQ
                VREKVFDYGRFRLAHELRG"
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promoter
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                4032..4060
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gene
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                4144..4428
                /gene="rplY"
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CDS
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                4144..4428
                /gene="rplY"
                /function="structural component; Ribosomal proteins -
                synthesis, modification"
                /note="o94; 100 pct identical to RL25_ECOLI SW: P02426"
                /codon_start=1
                /transl_table=11
                /product="50S ribosomal subunit protein L25"
                /protein_id="AAC75246.1"
                /db_xref="GI:1788512"
                /translation="MFTINAEVRKEQGKGASRRLRAANKFPAIIYGKGEAPLAIELDH
                DKVMNMQAKAEFYSEVLTIVDGKEIKVKAQDVQRHPVKPKLQHIDFVRA"
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repeat_region
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                4514..4547
                /note="REP (repetitive extragenic palindromic) element;
                contains 1 REP sequence"
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                complement(4567..5574)
                /gene="yejK"
                /note="b2186"
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                /function="orf; Unknown"
                /note="f335; 100 pct identical to YEJK_ECOLI SW: P33920"
                /codon_start=1
                /transl_table=11
                /product="orf, hypothetical protein"
                /protein_id="AAC75247.1"
                /db_xref="GI:1788513"
                /translation="MSLDINQIALHQLIKRDEQNLELVLRDSLLEPETVVEMVAELH
                RVYSAKNKAYGLFSEESELAQTLRQLRQROGEEDFLAFSRAATGRLRDELAKYPFADGGF
                VLFCHYRYLAVEYLLVAVLSNLSSMRVNENLDINPTHYLDINHADIVARIDLTEWETN
                PESTRYLTFLKGRVGRKVADFFMDFLGASEGLNAKAQNRGLLQAVDFTAEAQLDKAE
                RQNVRQQVSYCNELQQAGEEIELKSLSKELAGVSEVSFTEFAAEKGVELEESFPADR
                STLRQLTKFAGSGGGLTINFDAMLLGERIFWDPATDTLTIKGTPPNLRDQLQRRTSGG
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promoter
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                complement(5580..5608)
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                5707..5734
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promoter
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                5756..5983
                /note="factor Sigma70; predicted +1 start at 2282134"
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                5756..5983
                /gene="yejL"
                /note="b2187"
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CDS
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                /gene="yejL"
                /function="orf; Unknown"
                /note="o75; 100 pct identical to YEJL_ECOLI SW: P33921"
                /codon_start=1
                /transl_table=11
                /product="orf, hypothetical protein"
                /protein_id="AAC75248.1"
                /db_xref="GI:1788514"
                /translation="MPQISRYSDEQVEQLLAELLNVLEKHKAPTDLSLMVLGNMVTNL
                INTSIAPAQRQAIANSFARALQSSINEDKAH"
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gene
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                6003..7763
                /gene="yejM"
                /note="b2188"
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CDS
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                /gene="yejM"
                /function="putative enzyme; Not classified"
                /note="o586; 100 pct identical to YEJM_ECOLI SW: P33922"
                /codon_start=1
                /transl_table=11
                /product="putative sulfatase"
                /protein_id="AAC75249.1"
                /db_xref="GI:1788515"
                /translation="MVTHRQRYREKVSQMVSWGHWFALFNILLSLVIGSRYLFIADWP
                TTLAGRYSYVSIIGHFSFVPATYLLLFPLTFIVSGSQRLMRFLSVILATAGMTLL
                IDSEVFTRFHLHLNPIVWQLVINPDENEMARDWQLMFISVPVILLELVFATWSWQKL
                RSLTRRRFARPLAAFLFIAFIASHVVYIWADANFYRPITMQRANLPLSYPMTARRFL
                EKHGLLDAQEYORRLIEQGNPDAVSVQYPLSELRYRDMGTGQNVLLITVDGLSYSRFE
                KQMPALAGFAEQNISFTRHMSSGNTTDNGIFGLFYGISPSYMDGILSTRTPAALITAL
                NQQGYQLGLFSSDGFTSPLYRQALLSDFSMPSVRTQSDEQTATQWINWLGRYAQEDNR
                WFSWVSNGTNIDDSNQQAFARKYSRAGNVDDQINRVLNALRDSGKLDNTVVIITAG"
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RGIPLSEEETFDWSHGHLQVPLVIHWPGTPAQRINALIDHTDLMTTLMORLLHVSTP
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KPQLSLLLQVLTDEKRFIAN"

tRNA
7838..7914
/gene="proL"
/note="anticodon: GGG; CG Site No. 17629"
/product="tRNA-Pro"
/function="RNA; tRNA"

gene
7838..7914
/gene="proL"
/note="b2189"

gene
complement(8017..10527)
/gene="yejO"
/note="b2190"

CDS
complement(8017..10527)
/gene="yejO"
/function="putative transport; Not classified"
/note="f836; This 836 aa ORF is 99 pct identical to
836 residues of a 863 aa protein YEJO_ECOLI SW: P33924 but
contains -27 additional N-ter"
/codon_start=1
/transl_table=11
/product="putative ATP-binding component of a transport
system"
/protein_id="AAC75250.1"
/db_xref="GI:1788516"
/translation="MASTVEYGETVDGVVLEKDIQLVVGTANNTKINPGGEQHIKEFG
VSNNTEINGGYQYIEMNGAAEYSVLNDGYQIVQMGGAANQTLNNGVLQVYGAANDTT
IKGGRLIVEKDGGAVFVAIEKGLLEVKEGGFAFAVDQKAGGAIKTTTRAMEVFGTNR
LGQPDIKNGIANNMLLENGGSLRVEENDFAYNTTVDSGGLLEVMDGGTVTGVDKKAGG
KLIVSTNALEVSGCPNSRKGQFSIKDGVSKNYELDDGSGLIVMEDTQAIDTILDKHATMQ
SLGKDTGTKVQANAVYDLGRSYQNGSITYSSKAISENMVINNGRANVWAGTMVNVSR
GNDGILEVMKPQINYAPAMLVGKVVVSEGASFRTHGAVDTSKADVSLENSVWTIIADI
TTTNQNTLNLANLAMSDANVIMMDEPVTRSSVTASAENFITLTTNTLSGNGNFYMRT
DMANHQSDQLNVTGQATGDFKIFVTDTGASPAAGDSLTLVTTGGGDAAFTLGNAGGVV
DIGTYEYTLLDDNGNHSWSLAENRAQITPSTTDVLNMAAAQPLVFDAELDTVRERLGSV
KGVSYDTAMWSSAINTRNVVTDAGAGFEQTLTGLTLGIDSRFSREESSTIRGLIFGY
SHSDIGFDRGKGKGNIDSYTLGAYAGWEHQNGAYVDGVVKVDRFANTIHGKMSNGATAF
GDYNSNGAGAHVESGFRWVDGLMWSVRPYLAFTGFTTDGQDYTLSNGMRADVGNTRILR
AEAGTAVSYHMDLQNGTTLEPWLKAAVRQEYADSNQVKVNDDGKFNNDVAGTSGVYQA
GIRSSFTTPLSGHLSVSVGNGAGVESPWNTQAGVWTF"

promoter
10358..10386
/note="factor Sigma70; predicted +1 start at 2286786"

gene
10532..10654
/gene="b2191"

CDS
10532..10654
/gene="b2191"
/function="orf; Unknown"
/note="o40; This 40 aa ORF is 38 pct identical (1 gap)
to 41 residues of an approx. 384 aa protein ILEU_HUMAN SW:
P30740"
/codon_start=1
/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAC75251.1"
/db_xref="GI:1788517"
/translation="MGEYKEGANKRGNSSRLTQSFHHFMFEPIFSPVNALNQPI"

promoter
complement(10539..10568)
/note="factor Sigma70; predicted +1 start at 2286925"

repeat_region
complement(10692..11708)
/gene="trs5_8"
/note="b2192"

promoter
complement(10569..10597)
/note="factor Sigma70; predicted +1 start at 2286955"

gene
complement(10692..11708)
/gene="trs5_8"
/note="b2192"

CDS
complement(10692..11708)
/gene="trs5_8"
/function="IS, phage, Tn; Transposon-related functions"
/note="f338; 98 pct identical to YI52_ECOLI SW: P03837"
/codon_start=1
/transl_table=11
/product="IS5 transposase"

/protein_id="AAC75252.1"
/db_xref="GI:1788518"
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PWQNMVEVIEPFYPKAGNGRRPYPLETMLRIRHCMQHWYNLSDGAMEDALYEIASMRLF
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APSSTKNKEQQRDPEMHQYKKGNQWHFGMKAHIGVDAKSGLTHSLVTTAANEHDLNQL
GNLLHGEEQFVSADAGYQGAPQREELAEVDVDWLIAERPGVRTLKQHPRKNKTAINI
EYMKASIRAVEHPFRIIKRQFGFVKARYKGLLKNDQLAMLFTLANLFRADQMIRQW
ERSH"

promoter
complement(11817..11843)
/note="factor Sigma70; predicted +1 start at 2288203"

promoter
complement(11856..11886)
/note="factor Sigma70; predicted +1 start at 2288242"

promoter
11961..>11961
/note="factor Sigma70; predicted +1 start at 2288389"

BASE COUNT   2950 a   3186 c   2857 g   2968 t
ORIGIN

AE000308 Length: 11961   September 24, 2001 09:20 Type: N Check: 6916 ..

Initial Score   =   35   Optimized Score   =   302   Significance = -0.65
Residue Identity   =   51%   Matches   =   518   Mismatches   =   243
Gaps   =   115   Conservative Substitutions   =   0

```
                                                        x          10         20
                                            GCTAT-AATGCGGCAATTGATA
                                            ||||| |||||||||||||||||
AGTTGGTACACCAAAAGGCAAAAGTGACAACGTTCCGGTACAGGTTTTCTGCCCTGCCTGCGG-TTTTGCCA
3360       3370       3380       3390       3400       3410       3420

       30          40          50          60          70          80
ACGCCT------GAAA-TACC-ATGACGAAAACTTCTTTTAGAAAAACACCGGGTTGAGCGATTCAGCTCA
|| ||||      ||| |||| ||||||||||||| |||||||||||||||||||||     ||||||||||
ACACCTTTTGGGGAAAACGACCCGACGGGACATTGATT--GAACAC----TTTGGCTCGTCGTG-TCA
3430       3440       3450       3460       3470       3480       3490

      90         100         110         120         130         140        150
CGACAAGCCACCAGAAGAAACGGCCAG-AACCCCAGCCAACGCGGGT--CAT-ACTGTTCAATAAA---CCTAC
||||  ||||| || ||||||| |||| ||||||| ||||||| ||   ||| |||||| ||||||
GGGATAGTTTGAAGATG-ACGACGGTCATCGCGAACAAATGTGACTTCCGTTTCCGTTTAAAAATTGCCCGC
3500       3510       3520       3530       3540       3550       3560

       160         170         180         190         200         210       220
GATGTATTGCCCAGTTTACCGACGAGGCCGGCGGGCCTGAAG-GACTTTATCCCCGTACAGGGAGT
|||||  ||| |||| ||||||||| |||| ||| ||||  |  ||||||||||||||||| |||||
AATGTAACGCGGAA----AACGATATTGCCCGCCGC----CGCTGCCGGAATGTGACACCGTACTGGTTG-
3570       3580       3590       3600       3610       3620

         230         240         250         260         270         280
CTACGGCGGGACGTCTGGATCG------CGACAGCGAGGGGCTGCTGGCCTTAC-CAATGACGGCGTGC
||| |||| ||||| || ||||      |||| |||||| | | ||  ||||  ||||| ||||||||
ATCCGGA-CGATATGTTAAAGCGGGCGTAGCGGTCGCTGGT-ATTACGCTGTAGCGGCATG-
3630       3640       3650       3660       3670       3680       3690

      290         300         310         320         330         340       350
TCCAGGCCAGGTTACTCA-GCCGGGCAA-ACGTACCG-GAAAAATTTACTATGCAGGTTGAAGGCGAGC
|| ||| ||||| | || |  |||| || ||| | ||  |||||||||||||| |  || ||||||||
TCTTTGCAA--CATGGGCACCAGACGAAAAGGCGAATGGTTGAAAATCACCTAT-TAC--GATGAAGACGGCG
3700       3710       3720       3730       3740       3750       3760

         360         370         380         390         400         410
CGGACG------ACGCGT---GGCTGGCAA--AGCTGCGCAACGGCGTAACGC--TGAACGACGGTCCCACCC
|||| |       |||| |   |||||||||     ||||||||||||||||   ||||||||| ||||  ||
CGGATGTGAGTGAGCGTTTCCGTCTGCCAAACACCTGCCCA----GGCTACCCGCCTTCGCAGCAGTTTTATCC
3770       3780       3790       3800       3810       3820       3830

      420         430         440         450         460         470       480
TGCCGGCTGGTA-TTGAAC-GTGTGAATGAACCGAGTGGCTGGCTGGCCGCCGCCGCCGAT-TCGT-GAG
|| || ||     ||||| |  |  |  |||||||| |||||||||||||||||| ||||    ||| |||
-GCCCGC--ATACGCGACCACACGGGCAT---CCGCTGCGCTGGATCACCG---CCGCCATATCCTCGCGCC
3840       3850       3860       3870       3880       3890

490         500         510         520         530         540
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CGTAAATCC--ATTCCTACCAGCTGG--CTTAAAATCACCCTTTATG-AAGGCCGCAACCGACAGGT-----
  |||  |||  ||   ||||||||||  ||  ||||  |||||| ||| ||  |||||| || ||||| |||||
CAGCAAGCCTTATTGCGA-CACCCGGATTTTGTCGTCGCCC--GCATGAAAGGCCAGTACTGGCAGGTGCGTG
      3910        3920        3930        3940        3950        3960

                  550        560        570        580        590        600        610
--CAGGGCCATGACTGCGCCATGTGGGCTTC-CCTACCCTGCGACTCATTCGCTACGCCATGGGCAGCTATAC
  |||  |||||| |||||| ||||| || |||  ||  ||||||| ||||| |||||||| ||||||||||||
AAAAGTGTTGACGAAGGTCGTTTTCGTCTGGGCACGAAT--TACGC--GGTTAATGGTAGTTTT--
      3970        3980        3990        4000        4010        4020

                  620        630        640        650        660
GCTGGA-CTCGCTGGCAAACGGG----GAA--TGGCGGGATGTTAC---CCTAAGGAGAACTGA
  ||||  ||| |||  ||||||||    |||   ||||||||| |||   |||   |||||||| ||
GATTGATGTATAAGGCGATTGAGTACAGAATCTCGCCCCGCTTTTGCATACGCAAAGCAGATCACTTACCTGT
      4040        4050        4060        4070        4080        4090        4100

TGCTGGGTCGCCTGTAGCAGGATTAATTTAAGAGAGAAAGAAA
      4110        4120        4130        4140
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```
6. US-09-252-691C-1394 (1-669)
d90748      TOIG of: d90748      check: 3982      from: 1      to: 15007

TOIG of: d90748      check: 3982      from: 1      to: 15007

LOCUS       D90748      15007 bp      DNA              BCT       07-FEB-1999
DEFINITION  Escherichia coli genomic DNA. (25.6 - 25.9 min).
ACCESSION   D90748 AB001340
VERSION     D90748.1  GI:1651553
KEYWORDS    Complete and shotgun sequencing; potB; potA; pepT; phoQ; phoP;
            purB; ycfC; ycfB; icdA; icd; icdE; lit.
SOURCE      Escherichia coli(strain:K12) DNA, clone:Kohara clone #239.
ORGANISM    Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1 (sites)
AUTHORS     Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
            Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K.,
            Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T.,
            Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H.,
            Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K.,
            Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
TITLE       A 718-kb DNA sequence of the Escherichia coli K-12 genome
            corresponding to the 12.7-28.0 min region on the linkage map
JOURNAL     DNA Res. 3 (3), 137-155 (1996)
MEDLINE     97061202
REFERENCE   2 (sites)
AUTHORS     Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T.,
            Ikemoto,K., Inada,T., Isono,S., Itoh,T., Kanai,K.,
            Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Miki,T., Mori,H.,
            Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H.,
            Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T.,
            Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
            Yamamoto,Y. and Yano,M.
TITLE       The systematic sequencing of the Escherichia coli genome in Japan
JOURNAL     Unpublished (1996)
REFERENCE   3 (bases 1 to 15007)
AUTHORS     Mori,H.
TITLE       Direct Submission
JOURNAL     Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases.
            Hirotada Mori, NARA Institute of Science and Technology, Res. &
            Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
            Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
            Fax:81-7437-2-5669)
COMMENT     Collaboration Information:
            Project:
            The Japan E.coli genome DNA sequencing project
            Group:
            The Japan E.coli genome DNA sequencing group
            Members: (1995.4 - 1996.3)
            Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
            Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
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            Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
            Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K.,
            Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
            Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N.,
            Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
            Yamamoto,Y. and Yano,M.
            Headed by:
            Name: Takashi Horiuchi
            Address: National Institute of Basic Biology, Okazaki, 444, Japan
            E-mail: kishori@nibb.ac.jp
            Information operator:
            Name: Hirotada Mori
            Address: NARA Institute of Science and Technology,
                     Ikoma, 630-01, Japan
            E-mail: hmori@gtc.aist-nara.ac.jp
            URL:
            The Japan E. coli genome database
            http:bsw3.aist-nara.ac.jp.
FEATURES          Location/Qualifiers
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                                                                    TCTCTTCAACACGT--AAGTCTTCCGGGGCCA---GCAGAAC-ATGCA-GTTTTGCCGCCGTTCAACGGC-
                                                                    920                  930         940         950         960         970         980

                                                                    GGTATTGAACGT-GTGAATGAACCCGAGTGGCT-----GTGGCCGGCCAACCCGCCCGCCATTCGTGAGCGTAAA
                                                                    -|||||||  |||  |||-|| ||| || |||     ||-|| || |||||  |||||| || ||||||  |||
                                                                    -GAAGTTAACGTAGCTAGATATTACATTCGCG-GCCTTCAACGTGGCGCCG-TACGCGCTG-CTCGT----CTAGA
                                                                    990         1000        1010        1020        1030        1040

                                                                    TCCATTC-CTACCAGCTGGC-TTAAA-ATCACCCTTT-----ATGAAGGCCCGCAACCGACAGGTCAGGCGCA
                                                                    -||| |||-||||||  ||| ||||| |||||    | |   ||||||| |||  ||||||| ||||||  ||
                                                                    --CGTTCGATGCACAG-TGGCGTTAACATATTGATTTCGCCAATGAAGCCGCAATCGCCGACCAACAAACAGGTTTTTCGGC
                                                                    1050        1060        1070        1080        1090        1100        1110

                                                                    TGACTCGCCATGTGGGCTTC-CCTACCCTG-CGACTCATTCCTACG--CCAT-GGGCAGCTATACCGCTGGAC
                                                                    |-| |||||||||||||    || |||| ||| |||| ||||| |||  |||||  |||| ||||||||||
                                                                    T--CTTC-----GTAGATTTCACGCGGCGTGCCGTCTTGCTCAATGCCGACCATCGCCGACCACCACAAT--CC
                                                                    1120                1130        1140        1150        1160        1170
                                                                                                                                x
                                                                    TCGCTGGCAAACGGGAATG------GCGGGATGTTACCCCTAAGGAGAACTGA
                                                                    ||-| |||||||||||||     || |||||| |||| ||||||||| ||
                                                                    TGTCTG--ACATGGTGAGTGCTTCTTCCTGGTCGTGAGTCACAAAGACGAATGTAATGCCAAGCTTACGCTG
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                                                                    TAACGCTTTCAGCTCGTCGTTCTTGCATTGCTTAC
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TOIG of: d90749   check: 928   from: 1   to: 20284

LOCUS        D90749      20284 bp    DNA             BCT       07-FEB-1999
DEFINITION   Escherichia coli genomic DNA. (25.7 - 26.1 min).
ACCESSION    D90749 AB001340
VERSION      D90749.1  GI:1651562
KEYWORDS     Complete and shotgun sequencing; phoQ; phoP; purB; ycfC; ycfB;
             icdA; icd; icdE; lit; int; xis; ycfK; ycfE; pin; ycfA.
SOURCE       Escherichia coli(strain:K12) DNA, clone:Kohara clone #240.
ORGANISM     Escherichia coli
             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
             Escherichia.
REFERENCE    1 (sites)
AUTHORS      Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
             Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K.,
             Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T.,
             Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H.,
             Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K.,
             Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
TITLE        A 718-kb DNA sequence of the Escherichia coli K-12 genome
             corresponding to the 12.7-28.0 min region on the linkage map
JOURNAL      DNA Res. 3 (3), 137-155 (1996)
MEDLINE      97061202
REFERENCE    2 (sites)
AUTHORS      Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T.,
             Ikemoto,K., Inada,T., Isono,K., Itoh,T., Kanai,K.,
             Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M.,
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             Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T.,
             Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
             Yamamoto,Y. and Yano,M.
TITLE        The systematic sequencing of the Escherichia coli genome in Japan
JOURNAL      Unpublished (1996)
REFERENCE    3 (bases 1 to 20284)
AUTHORS      Mori,H.
TITLE        Direct Submission
JOURNAL      Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases.
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        AGIEWKADSADAEKVIKFLREEMGVKKIRFPEHCGIGIKPCSEEGTKRLVRAAIEYAI
        ANDRDSVTLVHKGNIMKFTEGAFKDWGYQLAREEFGGELIDGGPWLKVKNPNTGKEIV
        IKDVIADAFLQQILLRPAEYDVIACMNLNGDYISDALAAQVGGIGIAPGANIGDECAL
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CDS     14929..>15007
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ORIGIN

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Gaps                  =  100   Conservative Substitutions =            0
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||||-||||| || ||||| |||||||||||| -|||||||   || |||||||||| || |||||| ||||
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580                 590         600         610         620         630         640
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|  ||||||| |||  | || |||| |||  | |  |  | ||  ||||    ||||||  ||||||| |||
AACACAAGCCAACCGACAATAGTGACAATCAC-TACATTCTGGAACTTACTTGTTCTTGTTCTTCATCCAGTA
650                 660         670         680         690         700         710
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CGATGTATTGCCCGCAGTTTACCGACGAGGCCGGGCGCA--GCACGCTGAAGGACTTTATCCCCGTACAGG-G
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CGA--CCTCCCAGCTTCTACC--CAATTAATGGC-CATTTTTGGTCGCAGAGAGTGGTCAAAGT-CAGGAT
720               730         740         750         760         770         780
AGTCTACCGCAGCGGGACGTCTGGATCGGCGA-CAGCGAGGGGCTGCTGTGGT-CCTTACCAATGACGGCGTGCTCC
|||| ||   | | | |||||||||||||||| |  | ||  ||  |||||||  ||||||  |  |||||||| |
CGTCTTCATTG-AAGAATTC--GCTGACCACCATCTGC-CATTCAGCCCCTTACGC---CAATCAGCCCCTTCAGGTAAC-CAATCAGCCCCTTCAGCCG---ACTCC
790               800         810         820         830         840
                                    340         350
AG-GCCAGGC----TTACTCAGCCGGGCAAAACTACCGGAAAAATTTACTATGTGCAGGTTGAAGGCG---A
|  ||||||       |||||||| ||||  || | |||||||||  |||||||| |||||||||||||  |
AGCGTCATGCCCTTTGTAGTTACGCTCGCGAACGTAAC-CAATCAGCCCCTTCAGCGTAAC-TGGTTGTCGTCGTTAA
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360                 370         380         390         400         410         420
```

COMMENT   Hirotada Mori, NARA Institute of Science and Technology, Res. &
            Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
            Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
            Fax:81-7437-2-5669)
            Project:
             The Japan E.coli genome DNA sequencing project
            Group:
             The Japan E.coli genome DNA sequencing group
             Members: (1995.4 - 1996.3)
             Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
             Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
             Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
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             Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N.,
             Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
             Yamamoto,Y. and Yano,M.,
            Headed by:
             Name: Takashi Horiuchi
             Address: National Institute of Basic Biology, Okazaki, 444, Japan
             E-mail: kishori@nibb.ac.jp
            Information operator:
             Name: Hirotada Mori
             Address: NARA Institute of Science and Technology,
                      Ikoma, 630-01, Japan
             E-mail: hmori@gtc.aist-nara.ac.jp
            URL:
             The Japan E. coli genome database
             http:bsw3.aist-nara.ac.jp.
FEATURES   Location/Qualifiers
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        EISHVVLQHPLVTTAFSTQEREADSHATKWILGNLYESAPELKKRALGIATAVLCIQ
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        DVFKEAQHYGEVPGYNPALATKQPRRKITRQRLSLEEWKKIFDIADATHRYMGNAML
        LALVTGANYGEVPSAYLVHFFRSTSQAERGAQVKANTLTMNFSKARDLARIDWGEGSPATFHEQRS
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     Residue Identity  =   49%   Matches             =    361   Mismatches     =    268
                                 Gaps                 =   102   Conservative Substitutions   =     0

                                                               x          10
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                 TCGTGAAATATCGCGTTGCCATTAAAGGTCGCGTGACCACTCCGGTTGGTGCGGTATTCGCTCTGAACGT
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                   20        30        40        50        60        70        80
                 TG-ATAACGCTCGAAATACCATGACGAAAACTTCTTTTAGAAAACACCGGGTTGAGCGATTCAGCTCACGA
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                 TGCCCTGCGCCAGGAACT-GGATCTCTACATCTGCCT---GCGTCCGGTACGTT--ACTA-TCAGGGCACTC
                 6030      6040      6050      6060      6070      6080
                   90       100       110       120       130       140       150
                 CAAGCCACCAGAGAACGCCAGAACCCCAGCCAACGCGGGTCATACTGTTCAATAAACCTACCATGTAT-T
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                 CAAGCCCGGTTAAACAC--CCTGAA-CTGACCGA--TATGGTTATCTTCCGTGAAAACTCGGAAGACATTTAT
                 6090      6100      6110      6120      6130      6140      6150
                  160       170       180       190       200       210       220
                 GCCGCAGTTACCGACGAGGCCGGGGCCAGC--ACGCTG--AAG-GACTTTATCCC--CGTACAGGGAGTC
                 ||| || |||||||| |||||| |||||||  |||||  ||| |||||| |||||  ||| || |||||||
                 GCGG--GTATCGAATGGAAAGCAGACTCTGCCGACGCGCCAGAAAGTGATTAAATTCCTGCGTGAAGAGA-TG
                 6160      6170      6180      6190      6200      6210      6220
                  230       240       250       260       270       280
                 TACGCAGCGGGACGTCTGGATCGCG--ACAGCGAGGGGCTGCTGGTCCTTACCAATG-ACG---GCGTGCTC
                 |||| |||||||| |||||| |||  |||||||||||||||||| |||  |||||| |||   |||||||
                 GGGG-TGAAGAAATTCGCTTCCCGGAACATTGTGG--TATCGGTATTAAGCCGTGTTCGGAAGAAGGCAC
                 6230      6240      6250      6260      6270      6280      6290
                  290       300       310       320       330       340       350
                 C--AGGCCAGGCTTACTCAGCCGGGCAAACGTACCGGAAAAATTTACTAT-GTG-CAGGTTGA-AGGCGAGC
                 |  |||||||| |||||||| ||||| |||||| ||| |||||||| ||| ||| |||||| || |||||||
                 CAAACGTCTGGTTCGTCGCAG--CGATCGAA--TA-CGCAATTGCTAACGATCGGACGTCTGTGACTCTGTGC
                 6300      6310      6320      6330      6340      6350
                  360       370       380       390       400       410       420
                 -CGGACGACGCGTCGCTGGCAAAGCTGCGCAACGCACTGCCCAACGGCGTTAAAGACTGGGGCTACCAGCTGGCCGCGT
                 ||||||||| ||||||||  ||||||  |||  |||  |||||||||||| ||||| |||||||| |||||||||||||
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                 G--GTATTGAACGTGTGAA-TGAACCCGAGTGG-CTGTGGCCG------CGGAACCCGCCGATTCGTGAGCCG
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                 GAAGAGTTTGGCG-GTGAACGATCGACGGTGGCCGTGAAGTTAAAAACCCGAACACTGGCAA--A
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                 GAGATCGTCATTAAAGACGTGATTGCTGATGCCATTCGCAACA-GATCCTGCTGTGCCGGCCGTGAATATG-
                 6500      6510      6520      6530      6540      6550      6560
                  560       570       580       590       600       610
                 GCATGACTGGCGCATGTGGCTTCCCTACCCTGCGACT-CATTCGCTACGCCGGTG----GCAGCTATACGCT
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                 --ATGTTATCGGCCTGTATG--AACCTGAACGGTGACTACATTTCTGACGCCGGTATTGGCGCCGCAGGTTGCGGT
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CGAAATATGCCGGTCAGGACAAAGTAAATCCTGGCTCTA
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> O v
Ci, iD IntelliGenetics
> O v

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-252-691c-1394-inv.res made by sdavid on Mon 24 Sep 101 9:38:27-PDT.

Query sequence being compared:US-09-252-691C-1394' (1-669)
Number of sequences searched: 7
Number of scores above cutoff: 7

Results of the initial comparison of US-09-252-691C-1394' (1-669) with:
  File : portner691.seq

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100-

N  -
U  50-
M  -
B  -
E  -
R  -
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O  -
F  10-
   -
S  -
E  5-
Q  -
U  -
E  -
N  -
C  -       *
E  -    *
S  -
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SCORE 0    54   107   161   215   268   322   376   429   483
STDEV      0                                            1
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PARAMETERS

Similarity matrix	Unitary	
Mismatch penalty	1	
Gap penalty	1.00	K-tuple	4
Gap size penalty	0.33	Joining penalty	30
Cutoff score	0	Window size	32
Randomization group	0		

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	249	79	219.36

	CPU	Total Elapsed
Times:	00:00:00.99	00:00:01.00

Number of residues: 344036
Number of sequences searched: 7
Number of scores above cutoff: 7

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
				**** 1 standard deviation above mean ****		
1. ae000213	TOIG of: ae000213 check: 187	10959	483	498	1.07	0
2. d90748	TOIG of: d90748 check: 3982	15007	483	498	1.07	0
3. d90749	TOIG of: d90749 check: 928	20284	483	498	1.07	0
				**** 0 standard deviation from mean ****		
4. z99116	TOIG of: z99116 check: 4068	218470	110	317'	-0.63	0
5. ae000308	TOIG of: ae000308 check: 691	11961	78	291	-0.78	0
6. u00008	TOIG of: u00008 check: 8999	39149	78	291	-0.78	0
7. 109228	TOIG of: 109228 check: 8816	28206	33.	279	-0.98	0

1. US-09-252-691C-1394' (1-669)
   ae000213   TOIG of: ae000213 check: 1875 from: 1 to: 10959

TOIG of: ae000213 check: 1875 from: 1 to: 10959

LOCUS   AE000213   10959 bp   DNA   BCT   01-DEC-2000
DEFINITION Escherichia coli K12 MG1655 section 103 of 400 of the complete
            genome.
ACCESSION   AE000213 U00096
VERSION   AE000213.1 GI:1787371
KEYWORDS   .
SOURCE   Escherichia coli K12.
ORGANISM   Escherichia coli K12
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1 (bases 1 to 10959)
AUTHORS   Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau,B. and Shao,Y.
TITLE   The complete genome sequence of Escherichia coli K-12
JOURNAL   Science 277 (5331), 1453-1474 (1997)
MEDLINE   97426617
PUBMED   9278503
REFERENCE   2 (bases 1 to 10959)
AUTHORS   Blattner,F.R.
TITLE   Direct Submission
JOURNAL   Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   3 (bases 1 to 10959)
AUTHORS   Blattner,F.R.
TITLE   Direct Submission
JOURNAL   Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   4 (bases 1 to 10959)
AUTHORS   Plunkett,G. III.
TITLE   Direct Submission
JOURNAL   Submitted (13-OCT-1998) Laboratory of Genetics, University of
            Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
COMMENT   This sequence was determined by the E. coli Genome Project at the
            University of Wisconsin-Madison (Frederick R. Blattner, director).
            Supported by NIH grants HG00301 and HG01428 (from the Human Genome
            Project and NCHGR). The entire sequence was independently
            determined from E. coli K12 strain MG1655. Predicted open reading
            frames were determined using GeneMark software, kindly supplied by
            Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
            30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that
            have been correlated with genetic loci are being annotated with CG
            Site Nos., unique ID nos. for the genes in the E. coli Genetic
            Stock Center (CGSC) database at Yale University, kindly supplied by
            Mary Berlyn. A public version of the database is accessible
            (http://cgsc.biology.yale.edu). Annotation of the genome is an
            ongoing task whose goal is to make the genome sequence more useful
            by correlating it with other data. Comments to the authors are
            appreciated. Updated information will be available at the E. coli

Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of gene labels. This should allow them to be searched for in Entrez as gene names.

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                     /strain="K12"
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     promoter        13..40
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     protein_bind    119..136
                     /note="central position to predicted promoter:82"
                     /bound_moiety="PhoB predicted site"
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                     /note="b1127"
     CDS             155..1381
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                     /note="o408; 100 pct identical to 42 aa fragment
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                     IALGIGDEVLSPVMFPVLHQLLGQTLFITDGKTLLGADDKAGIAEIMTALAVLQQKKI
                     PHGDIRVAFTPDEEVGKAKHFDVDAFDARWAYTVDGGVGELEFENFNAASVNKIV
                     GNNVHPGTAKGVMVNALSLAARIHAEVPADESPEMTEGYEGFYHLASMKGTVERADMH
                     YIIRDFDRKQFEARKRKMMEIAKKVGKGLHPDCYIELVIEDSYNMREKVVEHPHILD
                     IAQQAMRDCDIEPELKPIRGGTDGAQLSFMGLPCPNLFTGGYNYHGKHEFVTLEGMEK
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                     /note="b1128"
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                     /note="o376; 100 pct identical to fragment YCFD_ECOLI
                     SW:P27431 but has 3 additional N-terminal aa and 93
                     additional C-terminal aa"
                     /codon_start=1
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                     VNVYPATSRMPKLTIVVVDTIPVELKSSYMWSWFIYVLSANLLLVIPLLWVAAWWSL
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                     /note="b1130"
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                     /note="f223; 100 pct identical to PHOP_ECOLI SW: P23836"
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     CDS             complement(4927..6297)
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                     /db_xref="GI:1787376"
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                     KVAEIPELHAVSEFIHFACTSEDINNLSHALMLKTARDEVLPYWRQLIDGIKDLAVQ
                     YRDIPLLSRTHGQPATPSTIGKEMANVAYRMEROYRQLNQVEILGKINGAVGNYNAHI
                     AAYPEVDWHQFSEEFVTSLGIQWNPYTTQIEPHDYIAELFDCVARFNTILIDFDRDVW
                     GYIALNHFKQKTIAGEIGSSTMPHKVNPIDFENSEGNLGLSNAVLQHLASKLPVSRWQ
                     RDLTDSTVLRNLGVGIGYALIAYQSTLGVSKLVNRDHLLDELDHNWEVLAEPIQTV
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                     /note="b1132"
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promoter      KGALDTIGNRINGLQRQLEHFDLQSETLMSAMAAIYVDVISPLGPRIQVTGSPAVLQS
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gene          /note="factor Sigma70; predicted +1 start at 1191348"
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              /gene="ycfB"
              /note="b1133"
CDS           complement(6978. .8129)
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              YQVEGLFMKNWBEDDGEEYCTAAADLADAQAVCDKLGIELHTVNFAAEYWDNVFELFL
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promoter      complement(7006. .7033)
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gene          /note="factor Sigma70; predicted +1 start at 1191911"
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CDS           complement(8138. .8599)
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              CCRWVSAEEILQASNLRSPLVAESIRCYQSGQRYPLEMIGDFNWPFTKGVI"
CDS           complement(8609. .9232)
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              /note="b1135"
              /gene="ymfC"
gene          complement(8609. .9232)
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              /function="orf; Unknown"
              /note="f207; This 207 aa ORF is 66 pct identical (1 gap)
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              P44827"
              /codon_start=1
              /transl_table=11
              /product="orf, hypothetical protein"
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              VEGIPTDALEALRNGVTLNDGPTLPAGAELVWREPAWLWPRNPPIRERKSIPTSWLKI
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promoter      9283. .9311
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gene          9434. .10684
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CDS           9434. .10684
              /gene="icdA"
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              KGALDTIGNRINGLQRQLEHFDLQSETLMSAMAAIYVDVISPLGPRIQVTGSPAVLQS
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              /protein_id="AAC74220.1"
              /db_xref="GI:1787381"
              /translation="MESKVVVPAQGKKITLQNGKLNVPENPIIPYIEGDGIGVDVTPA
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              LTTPVGGGIRSLNVALRQELDLYICLRPVRYYQGTPSPVKHPELTDMVIFRENSEDIY
              AGIEWKADSADAEKVIKFLREEMGVKKIRFPEHCGIGIKPCSEEGTKRLVRAAIEYAI
              ANRDSVTLVHKGNIMKFTEGAFKDWGYQLAREEFGGELIDGGPWLKVKNPNTGKEIV
              IKDVIADAFLQQILLRPAEYDVIACMNLNGDYISDALAAQVGIGIAPGANIGDECAL
              FEATHGTAPKYAGQDKVNPGSIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVTYD
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BASE COUNT    2685 a   2752 c   2819 g   2703 t
ORIGIN

AE000213  Length: 10959   September 24, 2001 09:14  Type: N  Check: 1875  ..

Initial Score        =   483   Optimized Score       =   498   Significance   =   1.07
Residue Identity     =    74%  Matches               =   504   Mismatches     =   163
Gaps                 =     8   Conservative Substitutions       =     0

                                                              x              10
                                                         TCAGTT---CTCCTT-AGGGGT
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8550      8560      8570      8580      8590      8600      8610

          20        30        40        50        60        70        80        90
AACATCCCGCCATTCCCGTTTGCCCAGCGAGTCCAGCGTATAGCTGCCATGGCCGTAGCGAATGAGTCGCAG
||||||||  |||||||  |||||||||||||| | |||||| |||||| |||| |||||||||||||||||
CACTTCTTCGCCATTCACCATTGGCAAGATTATCCAAAGAGTAATCACCCATCCATCCGAATCAGTCGCAG
8620      8630      8640      8650      8660      8670      8680

          100       110       120       130       140       150       160
GGTAGGGAAGCCACATGCGCAGTCATGCGCCTGACCTGTCGGTTGCGGCCTTCATAAGGGTGATTTTAAG
||| ||||| |||||||||||||||||||| ||| | |||| || |||||||||||||||||||||||||
CGTGGGGAAGCCAACATGGGCCGTCATGCGGCCGCGATTACGTCCTTCATATAAGGTGATCTTCAG
8690      8700      8710      8720      8730      8740      8750      8760

          170       180       190       200       210       220       230
CCAGCTGGTAGGAATGGAATTACGCTCACGAATCGGCCGGTTGCGCGGCCACTCGGTTCATTCAC
||||||||  |||||| |||||||||| ||||||||| ||||||||||||||||||||||||||||
CCAGCTGGTGGGAATACTTTCGCTTCACGAATTGGTGGATTCCGCGGCCATAACCACGCGGTTCGTCAAC
8770      8780      8790      8800      8810      8820      8830

          240       250       260       270       280       290       300
ACGTTCAATACCAGCCGGCCAGGGTGGGACCGTCGTTCAGCGTTACGCCGTTGCCGA--GCTTTGCCAGCGAC
||||  |||| |||||||||| |||||||||||||||||| |||||||| |||||||  ||||||||||||||
CAGCTCCGCGCCGCGGCCAGGGTAGGGCCATCATTTAAGGTTACGCCATTGCCAAGGCTTCAAGGCGTC
8840      8850      8860      8870      8880      8890      8900

          310       320       330       340       350       360       370
GCGTGCTCCGCGCTCGCCTTCAACCTGCCACATAGTAAATTTTTCCGGTACGTTGCCCGGCTAGTAAGCCTG
| |||||| | | |||||||||||||||||||||| |||||||||||| |||||||||||||||||||||||
TTGT-GT-GGGGATACCTTCCACCTGCACATATAGATTTTCCGGTCGTTCATGGGGTGCGTTAAACGC
8910      8920      8930      8940      8950      8960      8970

          380       390       400       410       420       430       440
GCCTGAGCACGCCGTCATTGTAAGGACCACCAGCCCGTCGGATCCAGACGTCCCGCTGCCTAG
||||||||||||| |||||||||||||||||||||||||| ||||| |||||||||||||||||
GCCTGCAACGCGCCGTTATTGGTCAGCACCAGCAACCCTTCGCTATCGGTCAAGGCGACCTGCATAA
8980      8990      9000      9010      9020      9030      9040

          450       460       470       480       490       500       510       520
ACTCCCTGTACGGGGATAAAGTCCTTCAGCGTGCTGCCGCCGGCCTCGTCGGCTAAACTGCGGCAATACATCG
|||||| ||||||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||
ACACCCCTGAACCGGGATGAATTCTTTAATGTTTGCGCCTGCTTCATCGCCGTGAACTGCGGAAGACAATCG
9050      9060      9070      9080      9090      9100      9110

          530       540       550       560       570       580       590
TAGGGTTTATTGAACAGTATGACCCCGTTGGCTGGGGTTCTCGGCGTTCTTCTTCTGGTGGCTTGCGTGGAGCTG
||||||||||||| |  ||||||||| |||||  |||||||||||| ||| |  ||||||||||||||||||||
TAGGGTTTATTGAACAGGATCACCAGCGCACGGCTGGCCTGGTTTTCAGTTTACGCCTTGGTAGAAGCGTTGCGAGCTG
9311      9283. .9311
```

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9120      9130      9140      9150      9160      9170      9180      9190
   600       610       620       630       640       650       660
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|||||| |||| |||| |||||||||| |||||||||||||||||||||| |||| |||||||||||||||
AATCGCTTAACCTGGTGATTTCTAAAAGAAGTTTTTGCATGGTATTTTTCAGAGATTATGAATTGCCGCATT
  9200      9210      9220      9230      9240      9250      9260

      X
ATAGC
|||||
ATAGCCTAATAACGCGCATCTTTCATGACGGCAAACAATAGGGTAGTATTGACAA
    9270      9280      9290      9300      9310
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2. US-09-252-691C-1394′ (1-669)
   d90748   TOIG of: d90748   check: 3982   from: 1 to: 15007

TOIG of: d90748   check: 3982 from: 1 to: 15007

LOCUS   D90748   15007 bp   DNA   BCT   07-FEB-1999
DEFINITION   Escherichia coli genomic DNA. (25.6 - 25.9 min).
ACCESSION   D90748 AB001340
VERSION   D90748.1 GI:1651553
KEYWORDS   Complete and shotgun sequencing; potB; potA; pepT; phoQ; phoP;
             purB; ycfC; ycfB; icdA; icd; icdE; lit.
SOURCE   Escherichia coli(strain:K12) DNA, clone:Kohara clone #239.
ORGANISM   Escherichia coli
             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
             Escherichia.
REFERENCE   1 (sites)
AUTHORS   Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
             Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K.,
             Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T.,
             Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H.,
             Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K.,
             Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
TITLE   A 718-kb DNA sequence of the Escherichia coli K-12 genome
             corresponding to the 12.7-28.0 min region on the linkage map
JOURNAL   DNA Res. 3 (3), 137-155 (1996)
MEDLINE   97061202
REFERENCE   2 (sites)
AUTHORS   Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T.,
             Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K.,
             Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M.,
             Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H.,
             Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T.,
             Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
             Yamamoto,Y. and Yano,M.
TITLE   The systematic sequencing of the Escherichia coli genome in Japan
JOURNAL   Unpublished (1996)
REFERENCE   3 (bases 1 to 15007)
             Mori,H.
TITLE   Direct Submission
JOURNAL   Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases.
             Hirotada Mori, NARA Institute of Science and Technology, Res. &
             Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
             Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
             Fax:81-7437-2-5669)
COMMENT   Collaboration Information:
             Project:
               The Japan E.coli genome DNA sequencing project
             Group:
               The Japan E.coli genome DNA sequencing group
             Members: (1995.4 - 1996.3)
               Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
               Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
               Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
               Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K.,
               Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
               Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N.,
               Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
               Yamamoto,Y. and Yano,M.
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Headed by:
  Name: Takashi Horiuchi
  Address: National Institute of Basic Biology, Okazaki, 444, Japan
  E-mail: kishori@nibb.ac.jp
Information operator:
  Name: Hirotada Mori
  Address: NARA Institute of Science and Technology,
           Ikoma, 630-01, Japan
  E-mail: hmori@gtc.aist-nara.ac.jp
URL:
  The Japan E. coli genome database
  http:bsw3.aist-nara.ac.jp.

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   d90749   check: 928   from: 1   to: 20284

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   DEFINITION   Escherichia coli genomic DNA. (25.7 - 26.1 min).
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   VERSION   D90749.1 GI:1651562
   KEYWORDS   Complete and shotgun sequencing; phoQ; phoP; purB; ycfC; ycfB;
                   icdA; icd; icdE; lit; int; xis; ycfK; ycfE; pin; ycfA.
   SOURCE   Escherichia coli(strain:K12) DNA, clone:Kohara clone #240.
   ORGANISM   Escherichia coli
                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                   Escherichia.
   REFERENCE   1 (sites)
   AUTHORS   Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
                   Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K.,
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                   Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
   TITLE   A 718-kb DNA sequence of the Escherichia coli K-12 genome
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   JOURNAL   DNA Res. 3 (3), 137-155 (1996)
   MEDLINE   97061202
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   AUTHORS   Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T.,
                   Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K.,
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                   Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H.,
                   Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T.,
                   Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
                   Yamamoto,Y. and Yano,M.
   TITLE   The systematic sequencing of the Escherichia coli genome in Japan
   JOURNAL   Unpublished (1996)
   REFERENCE   3 (bases 1 to 20284)
   AUTHORS   Mori,H.
   TITLE   Direct Submission
   JOURNAL   Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases.
                   Hirotada Mori, NARA Institute of Science and Technology, Res. &
                   Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
                   Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
                   Fax:81-7437-2-5669)
   COMMENT   Collaboration Information:
                   Project:
                       The Japan E.coli genome DNA sequencing project
                   Group:
                       The Japan E.coli genome DNA sequencing group

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Members: (1995.4 - 1996.3)
  Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
  Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
  Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
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  Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
  Yamamoto,Y. and Yano,M.
Headed by:
  Name: Takashi Horiuchi
  Address: National Institute of Basic Biology, Okazaki, 444, Japan
  E-mail: kishori@nibb.ac.jp
Information operator:
  Name: Hirotada Mori
  Address: NARA Institute of Science and Technology,
    Ikoma, 630-01, Japan
  E-mail: hmori@gtc.aist-nara.ac.jp
URL:
  The Japan E. coli genome database
  http:bsw3.aist-nara.ac.jp.

FEATURES             Location/Qualifiers
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          ANDRDSVTLVHKGNIMKFTEGAFKDWGYQLAREEFGGELIDGGPWLKVKNPTGKEIV
          IKDVIADAFLQQILLRPAEYDVIACMNLNGDYISDALAAQVGGIGIAPGANIGDECAL
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          EISHVVLQHPLVTTAFSTQEEREADSHATKWILGNLYESAPELKKRALGIATAVLCIQ
          SLEVENYFCLQNTHPAAYERIYSNISCYPVGNEELIEALCTVMLQYLFHGKNIVNLD
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gene      complement(10230..11357)
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          RDYAVSAYILVHFFRSTSQAERGAQVKANTLTMNFSKARDLARIDWGEGSSPATFHEQRS
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gene      complement(11338..11583)
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CDS       complement(11338..11583)
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CDS       14552..14731
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CDS       16282..16755
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CDS       16643..17473
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Residue Identity  =   74%     Matches                    =   504     Mismatches    =    163
Gaps              =     8     Conservative Substitutions =     0

                                                             10
                                                         x
                                  TCAGTT---CTTCTT-AGGGGT
                                  || ||    ||||| |  ||
                                                          4840      4850

       20        30        40        50        60        70        80        90
AAAATTGCCTTCTGCGTGCCACCAGCAACGTAAGCGTGGTTAAACATTTTGCATCCTTAATCTGT
 4790      4800      4810      4820      4830      4840      4850

AACATCCGGCCATTCCCCGTTTGCCAGCGAGTCCAGCGTATAGCTGCCATGGCGTAGCGAATGAGTCGCAG
||  || |||||||| || |||| |||||| ||||  ||||| || ||||||||||| |||||| |||||||
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4860      4870      4880      4890      4900      4910      4920

      100       110       120       130       140       150       160
GGTAGGGAAGCCACATGCGGCGTCATGCGCCTGACCTGTCGGTTGCGGCCTTCATAAAGGTGATTTTAAG
||||||||||| ||||| |||||| ||  || ||||||| |||| |  ||||||||||||||||||||||
CGTGGGGAAGCCAACATGGGCGGGTTCATGCGCCACCTGGCCATTACGTTACGGCCATTGCCAAGGTGCGTC
4930      4940      4950      4960      4970      4980      4990      5000

       170       180       190       200       210       220       230
CCAGCTGGTAGGAATGGATTTACGCTCACGAATCGGCGGGTTGCGCGGCCCACTCGGGTTCATTCAC
|||||||| |||||  |  |||||| |||||||| ||||||||| |||||||||| || |||||||||
CCAGCTGGTGGGAAATACTTTTGCGTTCACGAATTGGTGGATTCCCGCGGCCATAACCACGCGGGTTCGTCAAC
5010      5020      5030      5040      5050      5060      5070

       240       250       260       270       280       290       300
ACGTTCAATACCAGCGGCAGGGTGGGACCCGTCGTTCAGCGTTGCGCA--GCTTTGCCAGCGAC
|| |   |||||||||||||||||||||  ||||||||||||||||  |   |||| |||||||||
CAGCTCCGGCGGGGCAGGCAGGGTAGGGCCATCATTTAAGGTTACGGCCATTGCGCAAGGCTTCAAGTGCGTC
5080      5090      5100      5110      5120      5130      5140

       310       320       330       340       350       360       370
GGTCGTCCGGCTCGCTCCCTTCAACCTGCACATAGTAAATTTTTCCGGTACGTTTGCCCGGTCGAGTAAGCCTG
||||  |    ||||   |  ||||| ||||| || |  |  |||||||||||||| |||| || ||||
TTGT-GT-GGGAATACCTTCCACCTGCACATAATAGATTTTTTCCGGGTGGTTTACCCGGTCTGGGTTAAACGC
5150      5160      5170      5180      5190      5200      5210

       380       390       400       410       420       430       440
GCCTGGAGCACGCCGTCATTGGTAAGGACCAGCAGCCCCGCTGTCGTGCGATCAGCAGCCCTTCGCCGTAG
||||  |  |||||||| |||||||||||||||| |||| |  |||  |||||||||||| || |||| ||
GCCTGCAACGCGCCGTTATTGGTCGCAGCACCACGCAACCCTGCTATCGCGGTCAAGGCGACCTGCTGCATAA
5220      5230      5240      5250      5260      5270      5280

       450       460       470       480       490       500       510       520
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||||||  | ||||| ||||||| |   || |  |||| |||||  |||||  || | |||| |||| |||| ||| ||
ACACCCTGAACCGGATGAATTCTTTTAATGTTTGCGTCCGGTTCATCCGGATTTTCATGGTTTCAGAGATTTTCAGAAGAACATCG
5290      5300      5310      5320      5330      5340      5350

       530       540       550       560       570       580       590
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|| || |||| |||||||| |||| ||||||||||| | ||| | || | || |||| ||| |||||||||||
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5360      5370      5380      5390      5400      5410      5420      5430

       600       610       620       630       640       650       660
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|| || | ||| ||| ||||  ||  |||||||||||||||||| ||||||   |||||||| ||||| ||||||
AATCGCTTAACCTGGTGATTTTTCTAAAAGAAGTTTTTGCATGGTATTTTCAGAGATTATGAAGTTGCCGCATT
5440      5450      5460      5470      5480      5490      5500

                              x
                          ATAGC
                          ||||
ATAGCCTAATAACGGCCATCTTTCATGCACGGCAAACAATAGGGTAGTATTGACAA
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gene 18052..18681
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ORF_ID:o241#12
similar to PIR Accession Number S07956"
 /product="Hypothetical protein P-239"

gene complement(18788..19670)
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misc_feature 18812..19250
 /note="ORF is interrupted by frame-shifting
ORF_ID:o241#11
similar to SwissProt Accession Number P09154"
 /product="Very hypothetical 16.7 kd protein in
invertible-p region of excisable element e14."

gene complement(19670..20209)
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gene 20236..>20284
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4. US-09-252-691C-1394' (1-669)

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TOIG of: z99116  check: 4068  from: 1  to: 218470

LOCUS       BSUB0013   218470 bp    DNA             BCT       26-NOV-1997
DEFINITION  Bacillus subtilis complete genome (section 13 of 21): from 2395261
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ACCESSION   Z99116 AL009126
VERSION     Z99116.1  GI:2634723
KEYWORDS    .
SOURCE      Bacillus subtilis
  ORGANISM  Bacillus subtilis
            Bacteria; Firmicutes; Bacillus/Clostridium group;
            Bacillus/Staphylococcus group; Bacillus.
REFERENCE   1  (bases 1 to 218470)
  AUTHORS   Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G.,
            Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S.,
            Borriss,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C.,
            Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V.,
            Carter,N.M., Choi,S.-K., Codani,J.J., Connerton,I.F., Cummings,N.J.,
            Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoft,A., Ehrlich,S.D.,
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  TITLE     The complete genome sequence of the gram-positive bacterium
            Bacillus subtilis
  JOURNAL   Nature 390 (6657), 249-256 (1997)
  MEDLINE   98044033
REFERENCE   2  (bases 1 to 218470)
  AUTHORS   Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
            Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
            Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
            adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
            68 89 48
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                /transl_table=11
                /product="two-component sensor histidine kinase"
                /protein_id="CAB14243.1"
                /db_xref="GI:2634746"
                /db_xref="SWISS-PROT:P35164"
                /translation="MKFWKSVVGKLWFTILSLVLIVLFILTVLLLEFIENYHVEEAEN
                DLTQLANKVAVILENHEDQALARSITWELADNLTSIAIIQDEKNWYSPNDKNRLSSI
                TVEQIQHDKDLNKALKDHKKVSKRFGLSDFDTDNERLIVGVPYEKDGKKGMVFLSQSL
                LAVKDTTKHTTRYIFLAAGIAIVLITTFFAFFLSSRVTYPLRKMREGAQDLAKGKFDTK
                IPILTQDEIGELATAFNQMGRQLNFHINALNQEKEQLSNILSSMADGVITINIDGTIL
                VTNPPAERFLQAWYEQNMNIKEGDNLPPEAKELFQNAVSTEKEMIEMILQGRSWL
                LMSPLYAESHVRGAVAVLRDMTEERRLDKLREDFIANVSHELRTPISMLQGYSRAIVD
                DIASSEEDRKEIAQIIYDESLRMGRLVNDLLDLARMESGHTGLHYEKINVNEFLEKII
                RKFSGVAKENIALDHDISLTEEEFMFDEDKMEQVFTNLIDNALRHTSAGGSVSISVH
                SVKDGLKIDIKDSGSGIPEEDLPFIFERFYKADKARTRGRAGTGLGLAIVKNIVEAHN
                GSIITVHSRIDKGTTFSFYIPTKR"
gene            complement(21155. .21877)
                /gene="resD"
CDS             complement(21155. .21877)
                /gene="resD"
                /function="activation role in global regulation of aerobic
                and anaerobic respiration (resA, ctaA, qcrABC, fnr)"
                /note="alternate gene name: ypxD"
                /codon_start=1
                /transl_table=11
                /product="two-component response regulator"
                /protein_id="CAB14244.1"
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                /db_xref="SWISS-PROT:P35163"
                /translation="MDQTNETKILVVDDEARIRRLLRMYLERENYAIDEAENGDEAIA
                KGLEANYDLILDLMMPGTDGIEVCRQIREKKATPIIMLTAKGEEANRVQGFEAGTDD
                YIVKPFSPREVLRVKALLRRASQSYSFNANTPTKNVLVFSHLSIDHDAHRVTADGTE
                VSLIPKVYELLYFLAKTPDKVYDREKLLKEVWQYEFFGDLRTVDTHVKRLREKLNKVS
                PEAAKKIVTVWGVGYKFEVGAE"
gene            complement(21958. .23016)
                /gene="resC"
CDS             complement(21958. .23016)
                /gene="resC"
                /note="alternate gene name: ypxC"
                /codon_start=1
                /transl_table=11
                /product="essential protein similar to cytochrome c
                biogenesis protein"
                /protein_id="CAB14245.1"
                /db_xref="GI:2634748"
                /db_xref="SWISS-PROT:P35162"
                /translation="MGQHWNHPFYCRFFLPPRIFHHKVGCNGHAPVSNMFEFTTAFGM
                MLVLAFIILYFLYRLPSLGLFTLSTALLLIAYASMFPTDISPLIPSLQSNWLYIHVTT
                AALGQAILAISFVAGVFLLKHVDQTHPSKKTFWLEAIMFILVTTVAFIAITSAFRLA
                GYEAEFNWVDKSKEKSVMVYEMPALVGPHQGELLTEGRMEPLVDLPALFSGRKVNTVI
                WSFGAGLVLVGALRLIIRKRISALLHPLVKNVNLDLVDEVGYRAVSIGFPIFTLGALI
                FAMIWAQLAWTRFWGWDPKEVWALITFLFYAAYLHLRSRGWHGEKSAWLAVIGFAII
                MFNLIFVNLVLAGLHSYA"
gene            complement(23152. .24780)
                /gene="resB"
CDS             complement(23152. .24780)
                /gene="resB"
                /note="alternate gene name: ypxB"
                /codon_start=1
                /transl_table=11
                /product="essential protein similar to cytochrome c
                biogenesis protein"

                /protein_id="CAB14246.1"
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                /db_xref="SWISS-PROT:P35161"
                /translation="MKQVKCECGHINPVGTVLCESCGRALQETQPPLADMRYDGSARR
                SQTYNKTIIDKIWNFFSSVKVGIWLVITLAASAFGTIFPQEAYLPPGAQADTYYKEQ
                YGTFGQLYYLLGFHHLYGSWWYLLIASIGISLVICSLDRVIPLYRALKNQGVRRSPA
                FLRRQRLFSETVTVLNGESKEKIVTLLKKHYRIREKEGSILAEKGRFSRWGPYVNHI
                GLIIFLIGAMLRFVPGMYVDETLWVREGETAIPGTDGKYYLKNNQFSVETYNSKTEK
                KVFADAIDRVGDGRVAKNFQTDAVLYKREGKIVYGEKPKLEKVTEEDIRVNQPLRFDS
                FSVYQVDYKENOLDQMVFQLIDKTKKSFGSLKINLLDPDSVYDLGNGYKVEIASYLP
                DFYFNQDGEPSTKTKIPNNPAFVFNIITPDKPGEKSFVAIQETIEGSGNNKYKLKFD
                HVETKNITGLIVRKDLTLWVLAVGGAFMIGVIQGMYWQHRRIWLHSQDGAVMVAGHT
                NKNWFGLKKDLAFILADSGLTEPVDQKELIKTQK"
gene            complement(24777. .25322)
                /gene="resA"
CDS             complement(24777. .25322)
                /gene="resA"
                /note="alternate gene name: ypxA"
                /codon_start=1
                /transl_table=11
                /product="essential protein similar to cytochrome c
                biogenesis protein"
                /protein_id="CAB14247.1"
                /db_xref="GI:2634750"
                /db_xref="SWISS-PROT:P35160"
                /translation="MDNEEKAFIHSDRHPSRFNLRTRLYHLQRCICRQREYIRRSDA
                PNFVLEDTNGIKRIELSDLKGKGVFLNEWTWCEPCKKEFPYMANQYKHFKSQGVEIVA
                VNVGESKIAVHNFMKSYGVNFPVVLDTDRQVLDAYDVSPLPTTFLINPEGKVKVVTG
                TMTESMIHDYMNLIKPGETSG"
gene            complement(25454. .26143)
                /gene="ypuL"
CDS             complement(25454. .26143)
                /gene="ypuL"
                /function="unknown"
                /note="similar to hypothetical proteins"
                /codon_start=1
                /transl_table=11
                /protein_id="CAB14248.1"
                /db_xref="GI:2634751"
                /db_xref="SWISS-PROT:P35159"
                /translation="MERLQKYIAHAGVASRSKAEELIKEGKVKVNGKVVTELGVKVTG
                SDQIEVNGLKVEREEPVYFLLYKPRGVISAAQDDKGRKVVTDFFKNIPQRIYPIGRLD
                YDTSGLLLTNDGEFANKLMHPKYEIDKTYAAVKGIPPKELLRKLERGIRLEEGKTA
                PAKAKLLSLDKKQTSIQLTIHEGRNRQVRRMFEAIGHEVILKREEYAFLNLRGLH
                TGDARELRLTK"
gene            complement(26227. .26774)
                /gene="spmB"
terminator      complement(26227. .26241)
                /gene="spmB"
CDS             complement(26235. .26774)
                /gene="spmB"
                /function="required for spore core dehydration"
                /note="alternate gene name: ypuK"
                /codon_start=1
                /transl_table=11
                /product="spore maturation protein"
                /protein_id="CAB14249.1"
                /db_xref="GI:2634752"
                /translation="MEIINWLSLAMIPIIAGILLYGTIKKVPVTYESFVEGGKEGIEI
                AFSHYPLFSRNACRYNCFQIHPGALDFIMDLKPAFSAIGIPAEVVPLALIRPISGTA
                ALGMTTDLIAVYGPDSFIGRLASVMQGSTDTTLYVLTVYFGAVGIKKMGDALKVGLLA
                DLIGVVASIIIVTLLFGSA"
gene            complement(26779. .27369)
                /gene="spmA"
CDS             complement(26779. .27369)
                /gene="spmA"
                /function="required for spore core dehydration"
                /note="alternate gene name: ypuJ"
                /codon_start=1
                /transl_table=11
                /product="spore maturation protein"
                /protein_id="CAB14250.1"
                /db_xref="GI:2634753"
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gene
CDS
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                /translation="MVNIIWVSLTVIGLVFAMCNGTLQDVNEAVFKGAKEAITISFGL
                MSVLVFWLGLMKIAEQSGLLDIFSRMCRPFISKLFPDIPPDHPAMGYILSNLMANFFG
                LGNAATPLGIKAMEQMKKLNGNRSEASRSMITFLAVNTSCITLIPTTVIAVRMAYSSK
                TPTDIVGPSILALLISGIGAIIDRYFYYRRKKGR"
     complement(27357..28505)
                /gene="dacB"
     complement(27357..28505)
                /gene="dacB"
                /EC_number="3.4.16.4"
                /function="required for spore cortex synthesis
                (peptidoglycan biosynthesis)"
                /codon_start=1
                /transl_table=11
                /product="D-alanyl-D-alanine carboxypeptidase
                (penicillin-binding protein 5*)"
                /protein_id="CAB14251.1"
                /db_xref="GI:2634754"
                /db_xref="SWISS-PROT:P35150"
                /translation="MRIFKKAVFVIMISFLIATVNVNTAHAAIDVSAKSAIIIDGASG
                RVLYAKDEHQKRRIASIFKIMTAVLAIESGKMDQTVTVSANAVRTEGSAIYLTEGQKV
                KLKDLVYGLMLRSGNDAAVAIAEHVGGSLDGFVYMMNQKAEQLGMKNTRFQNPHGLDD
                HENHYSTAYDMALLTKYAMKLKDYQKISGTKIYKAETMESVWNKNKNLLTMLYPYSTG
                GKTCYTKLAKRTLVSTASKDGIDLIAVTINDPWDDHMKMFNYVFEHYQTYLIAKKG
                DIPKIKGTFYESKAFIKRDITYLLTEEEKNVKINTTLLKPKKAWEKDASKIPDIVGH
                MEIMFNDATIAKVPIYYENERHQKPKKQFFETFKSIFLNAAGAKWSI"
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terminator
gene
CDS
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                /gene="ypuI"
     complement(28601..29167)
                /gene="ypuI"
     complement(28628..29167)
                /gene="ypuI"
                /function="unknown"
                /note="similar to hypothetical proteins from B. subtilis"
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                /transl_table=11
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                /db_xref="SWISS-PROT:P35156"
                /translation="MKEAKCERQIHEGKIPNEMGHSIVRAQTQKTGEFLSMVVNTVND
                YLNQTTLESLQAELPIERGYCCDVLSTLRRMAVFCEGGAEACRRLLMOEPFQEARAEK
                TLYNVYHQCIEEFFMPKKDTWCENSRASYTGVSAIEFYHAVPASLEQLLPLSAAFLK
                MREELAHYEASGSSMAPIR"
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gene
CDS
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                /function="unknown"
                /note="similar to hypothetical proteins"
                /codon_start=1
                /transl_table=11
                /protein_id="CAB14253.1"
                /db_xref="GI:2634756"
                /db_xref="SWISS-PROT:P35155"
                /translation="MGLDIVNWKAIVEALLYAAGDEGLITVLEEEPELNTIM
                ADVADEYRGDTRGIELIEYADTYMLSTRKDFAPYLKKLIEVPSKGLSQASLEVLAIVS
                YKQPITRAEIEEIRGVKSERILHSLVAKALLCEVGRADGPGRAILYGTTPTFLEQFGL
                KTLDELPPLPENAEEDVLQEEADLFFENFNQTFEDIK"
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gene
CDS
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                /function="unknown"
                /note="similar to hypothetical proteins"
                /codon_start=1
                /transl_table=11
                /protein_id="CAB14254.1"
                /db_xref="GI:2634757"
                /db_xref="SWISS-PROT:P35154"
                /translation="MEEYQVKIDTFEGPLDLLLHLINRLEIDIYDIPVAKITEQYLLY
                VHTMRVLEDIASEYLVMAATLLSIKSRMLLPKQEEELFEDELLEEEDPREELIEKLI
                EYRKYKDAAKDLKEREEERQKSFTKPPSDLSEYAKEVKQSEQKLSVTVDMIGAFQKV
                LKRKINRPRMETTITRQDIPIEARMEIVHSLKSRGTRINFMDLFPYEQKEHLVVTFL
                AVLELMKNQLVLIEQEHNFSDIYITGSESIHGA"
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gene
CDS
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     30841..31365
                /gene="ypuF"
     30841..31365
                /function="unknown"
                /codon_start=1
                /transl_table=11
                /protein_id="CAB14255.1"
                /db_xref="GI:2634758"
                /db_xref="SWISS-PROT:P17617"
                /translation="MYPKAYIDYLVFEHATRDYFECHEILEEYWKEDPPKKRKRYWVG
                FIQLAVALYHRRONTAGAKRLMANSIRILQAEHRAVEDLGLDHGRLLELMOSVYEQI
                ETVSAYKSIILPIKDEKLEEACRIECRKKKYTWGQPSALSNIFLIDKHRLRDRTDVIR
                EREKEIERRKKSRD"
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terminator
gene
CDS
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                /gene="ribT"
     complement(join(31355..31378,31379..31753))
                /gene="ribT"
     complement(31379..31753)
                /gene="ribT"
                /function="riboflavin biosynthesis"
                /note="alternate gene name: ribD"
                /codon_start=1
                /transl_table=11
                /product="reductase"
                /protein_id="CAB14256.1"
                /db_xref="GI:2634759"
                /db_xref="SWISS-PROT:P17622"
                /translation="MLIRYKKSFEKIAMGLLSFMPNEKDLKQLOQTIKDYETDTDRQL
                FLWKEDEDIVGAIGVEKKDSEVEIRHISVNPSRHQGIGKQMMDALKHLFKTQVLVPN
                ELTQSFFERCGQOQDISYNN"
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gene
CDS
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                /gene="ribH"
                /function="riboflavin biosynthesis"
                /codon_start=1
                /transl_table=11
                /product="riboflavin synthase (beta subunit)"
                /protein_id="CAB14257.1"
                /db_xref="GI:2634760"
                /db_xref="SWISS-PROT:P11998"
                /translation="MNIIQGNLVGTGLKIGIVVGRFNDFITSKLLSGAEDALLRHGVD
                TNDIDVAWVPGAFEIPFAAKKMAETKKYDAIITLGTVIRGATTHYDVCNEAAKGIAQ
                AANTTGVPVIPGIVTTENIEQAIERAGTKAGNKGVDCAVSAIEMANLNRSFE"
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gene
CDS
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     complement(32363..33559)
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                /gene="ribA"
                /EC_number="3.5.4.25"
                /function="riboflavin biosynthesis"
                /codon_start=1
                /transl_table=11
                /product="GTP cyclohydrolase II and
                3,4-dihydroxy-2-butanone 4-phosphate synthase"
                /protein_id="CAB14258.1"
                /db_xref="GI:2634761"
                /db_xref="SWISS-PROT:P17620"
                /translation="MFHPIEEALDALKKGEVIIVDDEDRENEGDFVALAEHATPEVI
                NFMATHGRGLICTPLSEEIADRLDLHPMVEHNTDSHHTAFTVSIDHRETKTGISAQER
                SFTVQALLDSKSVPSDFQRPGHIFPLIAKKGGVLKRAGHTEAAVDLAEACGSPGAGVI
                CEIMNEDGTMARVPELIEIAKKHQLKMITTIKDLIQYRYNLTLVEREVDITLPTDFGT
                FKVYGYTNEVDGKEHVAFVMGDVPFGEGPLVRVHSECLTGDVFGSHRCDCGPQLHAA
                LNQIAAEGRGVLLYLRQEGRGIGLINKLAYKLQEQGYDTVEANEALGFLPDLRNYGI
                GAQILRDLGVRNMKLLTNNPRKIAGLEGYGLSISERVPLQMEAKEHNKKYLQTKMNKL
                GHLLHF"
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gene
CDS
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     complement(33574..34221)
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     complement(33574..34221)
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                /EC_number="2.5.1.9"
                /function="riboflavin biosynthesis"
                /codon_start=1
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gene                  /transl_table-11
                      /product="riboflavin synthase (alpha subunit)"
                      /protein_id="CAB14259.1"
                      /db_xref="GI:2634762"
                      /db_xref="SWISS-PROT:P16440"
CDS                   /translation="MFTGIIEETGTIESMKKAGHAMALTIKCSKILEDVHLGDSIAVN
                      GICLIVTDFTKNQFTVDVMPETVKATSLNDLTKGSKVNLERAMAANGRFGGHFVSGHV
                      DGTAEITRIEEKSNAVYYDLKMDPSLTKTLVLKGSITVDGVSLIIFGLIEDTVISLI
                      PHTISETIFSEKTIGSKVNIECDMIGKYMYRFLHKANENKTQQTITKAFLSENGF"
gene                  complement(34232. .35317)
                      /gene="ribG"
CDS                   complement(34232. .35317)
                      /gene="ribG"
                      /function="riboflavin biosynthesis"
                      /codon_start-1
                      /transl_table-11
                      /product="riboflavin-specific deaminase"
                      /protein_id="CAB14260.1"
                      /db_xref="GI:2634763"
                      /db_xref="SWISS-PROT:P17618"
                      /translation="MEEYYMKLALDLAKQGEGQTESNPLVGAVVVKDGQIVGMGAHLK
                      YGEAHAEVHAIHMAGAHAEGADIYVTLEPCSHYGKTPPCAELIINSGIKRVFVAMRDP
                      NPLVAGRGISMMKEAGIEVREGILADQAERLNEKFLHFMRTGLPVVTLKAAASLDGKI
                      ATSTGDSKWITSEAARQDAQOYRKTHQSILVGVGTVKADNPSLTCRLPNVTKQPVRVI
                      LDTVLSIPEDAKVICDQIAPTWIFTTARADEDEKKVLSAFGVNIFTLETERIQIPDVL
                      KILABEGIMSVYVEGGSAVHGSFVKEGCFQEIIFYFAPKLIGGTHAPSLISGEGEFQSM
                      KDVPLLQFTDITQIGRDIKLTAKPYKE"
gene                  complement(35299. .35451)
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CDS                   complement(35299. .35451)
                      /gene="ypuE"
                      /function="unknown"
                      /codon_start-1
                      /transl_table-11
                      /protein_id="CAB14261.1"
                      /db_xref="GI:2634764"
                      /db_xref="SWISS-PROT:P35153"
                      /translation="MMSRYAKCLKMHSVISYCVKYLKPRIFYKFGAFLTVNNKRGEGN
                      KWKSII"
terminator            complement(35679. .35705)
                      /gene="ypuD"
gene                  complement(35679. .36054)
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CDS                   complement(35710. .36054)
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                      /function="unknown"
                      /codon_start-1
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                      /db_xref="GI:2634765"
                      /db_xref="SWISS-PROT:P17616"
                      /translation="MGRIKTKITILLVLLLLAGGYMYINDIELKDVPTAIGQTLSSE
                      EEEYTIQEYKVTKIDGSEYHGVAENGTKIIFNGKKLNQDLSDIKEGDKIKAYFSKSKR
                      IDGLIKVAKVND"
terminator            complement(36262. .36282)
                      /gene="sipS"
gene                  complement(36262. .36843)
                      /gene="sipS"
CDS                   complement(36289. .36843)
                      /gene="sipS"
                      /EC_number="3.4.21.89"
                      /function="modulation of the capacity and specificity for
                      protein secretion"
                      /codon_start-1
                      /transl_table-11
                      /product="type I signal peptidase"
                      /protein_id="CAB14263.1"
                      /db_xref="GI:2634766"
                      /db_xref="SWISS-PROT:P28628"
                      /translation="MKSENVSKKKSILEWAKAIVIAVVLALLIRNFIFAPVVDGDSM
                      YPTLHNRERFVNMTVKYIGEFDRGDIVVLNGDDVHYVKRIIGLPGDTVEMKNDQLYI
                      NGKKVDEPYLAANKKRAKQDGFDHLTDDFGPVKVPDNKYFVMGDNRRNSMDSRNGLGL
                      FTKKQIAGTSKFVFYFNEMRKTN"

gene                  37110. .37346
                      /gene="ypzC"
CDS                   37110. .37346
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                      /function="unknown"
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                      /db_xref="GI:2634767"
                      /db_xref="SPTREMBL:032012"
                      /translation="MFIYCIPLISQSMIPMALDKTINVMKVTGMFAATYFTGDNRTPF
                      FAFIICLKSFKLENMDQPPKNKSNIFPAVEDSLL"
gene                  complement(37749. .38138)
                      /gene="ypuC"
CDS                   complement(37749. .38138)
                      /gene="ypuC"
                      /function="unknown"
                      /codon_start-1
                      /transl_table-11
                      /protein_id="CAB14265.1"
                      /db_xref="GI:2634768"
                      /db_xref="SWISS-PROT:P35152"
                      /translation="MSYWIGYRLGPAAIQKAFASRGVLLAVIVLTFWTVFRGQDRKI
                      ELSFLFIVIGGELYEEGIRRLFHSLHPVHAPLESHVLYPPFSEQTLTAFVIFGFCAY
                      LFVRHSHKTRLQTVWIFTLETFCLLSFYSSSG"
gene                  complement(38116. .38319)
                      /gene="ypuB"
CDS                   complement(38116. .38319)
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                      /function="unknown"
                      /codon_start-1
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                      /db_xref="GI:2634769"
                      /db_xref="SWISS-PROT:P35151"
                      /translation="MQVLTGLLEQYGYAVLFIVLMLELLALLGPGEPAGVLVFQEKLN
                      WVLSMLAAGLGLGSCGSEHVVLDRV"
gene                  38985. .39197
                      /gene="ypzD"
CDS                   38985. .39197
                      /gene="ypzD"
                      /function="unknown"
                      /note="similar to hypothetical proteins from B. subtilis"
                      /codon_start-1
                      /transl_table-11
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                      /db_xref="GI:2634770"
                      /db_xref="SPTREMBL:032013"
                      /translation="MIDYPININNVSGNSVINVGGAFMIRPLTLSKSVFGSGGLNTGI
                      VFENNFVSKAKMINHQFTDQNVTKTF"
gene                  complement(39298. .39764)
                      /gene="ppiB"
terminator            complement(39298. .39318)
                      /gene="ppiB"
CDS                   complement(39333. .39764)
                      /gene="ppiB"
                      /EC_number="5.2.1.8"
                      /note="alternate gene name: cypBS"
                      /codon_start-1
                      /transl_table-11
                      /product="peptidyl-prolyl isomerase"
                      /protein_id="CAB14268.1"
                      /db_xref="GI:2634771"
                      /db_xref="SWISS-PROT:P35137"
                      /translation="MKTGYFLLEDGNKIEFELYPEAAPGTVANFEKLANEGFYDGLTF
                      HRVIPGFVSQGGCPHGTGTGGPGYTIKCETEGNPHTHEAGALSMAHAGKDTGGSQFFI
                      VHBPQPHLNGVHTVFGKVTSGLEFAKNMSNGDVMKEVRVEG"
gene                  40018. .40912
                      /gene="ypuA"
CDS                   40018. .40890
                      /gene="ypuA"
                      /function="unknown"
                      /codon_start-1
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                 /transl_table=11                                                      /codon_start=1
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                 /db_xref="SWISS-PROT:P31847"                                          /db_xref="GI:2634776"
                 /translation="MKKIWIGMLAAAVLLMVPKVSLADAAVGDVIVTLGADLSESDK     /translation="MKLTGKQTWVFEHPIFVNSAGTAAGPKEKDGPLGSLFDKTYDEM
                 QKVLDEMNVPDNATVTVTNKEEHEYLGKYISNAQIGSRAISSSITIAKKGSGLNVE      HCNQKSWEMAERQLMEDAVNVALQKNLTKDDIDLLLAGDLLNQVTANYVARHLKIP
                 THNISGITDEMYLNALMTAGVKDAKVYYTAPFEVSGTAALTGLIKAYEVSSDEAISED    FLCMPGACSTSMETVAVASALVDGFAKRALAATSSHNATAERQFRYPTEYGGQKPDT
                 VKQVANQELVTTSELGDKIGNENAAALIAKIKEEFAKNGVPDNKADIEKQVDDAASDL    ATSTVTGSGAVVISQTPGDIQITSATVGKVSDLGITDPFDMGSAMAPAAADTIKQHFK
                 NVTLLTDSQKNQLVSLFNKMKNADIDWGQVSDQLDKAKDKITKFIESDECKNFIQKVID   DLNRTADDYDLILTGDLSGVGSPIVKDILKEDGYPVTKHDDCGLLIYTPDQQVFAGG
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                 /gene="ypuA"                                                  GGAS"
terminator       40897..40912
gene             complement(40919..42238)                          gene    complement(45775..46227)
                 /gene="lysA"                                               /gene="spoVAC"
CDS              complement(40919..42238)                          CDS     complement(45775..46227)
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                 /EC_number="4.1.1.20"                                      /note="mutants lead to the production of immature spores
                 /function="lysine biosynthesis"                            (stage V sporulation)"
                 /codon_start=1                                             /codon_start=1
                 /transl_table=11                                           /transl_table=11
                 /product="diaminopimelate decarboxylase"                   /protein_id="CAB14274.1"
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                 /db_xref="SWISS-PROT:P23630"                               FYIHFFDFNEKTAGNPTAATLLISALLTGFGIYDRIGQFAGAGSAVPVTGFANSMAS
                 /translation="MFLHGTSRONQHGHLEIGGVDALYLAEKYGTPLVYDVALIRER     AALEYKSEGLVLGVATNMFKLAGNVIVFGVVAAYIVGMIRFAFEKLMS"
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                 ERIHFHGNNKSREELRMALEHRIGCIVVDNFYETALLEDLCKETGHSIDVLLRITPGV   gene    complement(46239..46664)
                 EAHTHDYITTGQEDSKFGFDLHHNGQTERAIEQVLQSEHIQLLGVHCHIGSQIPDTAGF          /gene="spoVAB"
                 VLAAEKIFKKLDEWRDSYSFVSKVLNLGGFGIRYTEDDEPLHATEYVEKIIEAVKEN   CDS     complement(46239..46664)
                 ASRYGFDIPEIWIEPGRSLVGDAGTTLYTVGSQKEVPGVRQYVAVDGGMNDNIRPALY           /gene="spoVAB"
                 QAKYEAAAANRIGEAHDKTVSIAGKCCESGDMLIWDIDLPEVKEGDLLAVFCTGAYGY           /note="mutants lead to the production of immature spores
                 SMANNYNRIPRPAVVFEVENGEAHLVVKRETYEDIVKLDLPFKTGVKQ"                   (stage V sporulation)"
gene             complement(42344..43822)                                   /codon_start=1
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CDS              complement(42344..43822)                                   /protein_id="CAB14275.1"
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                 /note="mutants lead to the production of immature spores    /translation="MIVSVLFIIFVGLGGGITVGAGFVAFLTVMGIIPRLMQLTKTMR
                 (stage V sporulation)"                                      FVQAYEAAVILGAVCGGWETLHMNHLYTKWIAVPVGLLAGLFVGMLAAALTEVLNVL
                 /codon_start=1                                              PILAKRIGLRSKIIILLMAIVIGKIAGSLFHWLYFIDHS"
                 /transl_table=11
                 /protein_id="CAB14271.1"                                   gene    complement(46674..47276)
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                 /translation="MPDHKEEKIRVYRNPAKNEEYFKNRVGMGTSYDVGVRKLTILDK   CDS     complement(46674..47276)
                 EIQLYLNGLCDTAYIIHLMRELVAINNRKEDDPELVDIVENRLLNAQVEKVKTLDET            /gene="spoVAA"
                 TDQVLSGLVAVIVEGAGFAFIIDVRSYPGRNPEEPDTEKVVRGARDGFVENIVVNTAL           /note="mutants lead to the production of immature spores
                 LRRRIRDERLRVKMTKVGERSKTDLSICYIEDIADPDLVEIVKEIASIDVDGLTMAD            (stage V sporulation)"
                 KTVEEFIVNQSYNPFPLVRYTERPDVAANHVLEGHVIIIVDTSPSVIITPTTLFHHVQ           /codon_start=1
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                 WPLIPFGKALMVQLVRTAKPGAKVRPSIVHPKNRLRQPTNS"                   /translation="MMERRIFIRLRHRVLAHPGDIITVGDAAQIEGQLQLKKKLSAMP
gene             complement(43773..44744)                                   LYQVSEKDKNIVLLDIIQVLRAIHLQDPTIDVQTVGGAETIVEIQYRKRNLSTVLFIG
                 /gene="spoVAE"                                              WLLLFIGSCLAIMNFHEDVSMRDVHIALYEIITGERNDYPYLLQIPYSIGLGLGMIV
CDS              complement(43773..44744)                                   FFNHIFKKLNEEPARWRLRCLTISLSINWPCMRIKKP"
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                 /note="mutants lead to the production of immature spores   gene    complement(47398..48165)
                 (stage V sporulation)"                                             /gene="sigF"
                 /codon_start=1                                             CDS     complement(47398..48165)
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                 /protein_id="CAB14272.1"                                           /function="early forespore-specific gene expression"
                 /db_xref="GI:2634775"                                              /note="alternate gene name: spoIIAC"
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                 FGITYDKFIEFAGGGAIVPIVSFGHSLLHGAMHQAHIHGFIGIGMGIFELTSAGISAAI         /transl_table=11
                 LFAFIVAVIFKAERISADMTTKRKVILVTDGDVYAAKTIEYAASKVGRCISOSKGNP          /product="RNA polymerase sporulation-specific sigma factor
                 STRSGAELVKLIASAPYDRNGEITEYGVGEREFDRHMSGDTVVCLDKLDLPLTIGIG           (sigma-F)"
                 DIGKMGRKDDISKGSPITMKAVEFILERSGYHAGPQGRENSGLSESS"                    /protein_id="CAB14277.1"
gene             complement(44746..45762)                                   /db_xref="GI:2634780"
                 /gene="spoVAD"                                             /db_xref="SWISS-PROT:P07860"
CDS              complement(44746..45762)                                   /translation="MDVEVKKNGKNAQLKDHEVKELIKQSONGDQQARDLIEKNMRL
                 /gene="spoVAD"                                              VWSVVQRFLNRGYEPDDLFQIGCIGLLKSVDKFDLYDVRFSTYAVPMIIGBIQRFIR
                 /note="mutants lead to the production of immature spores    DDGTVKVSRSLKELGNKIRRAKDELSKTLGRVPTVQEIADHLEIEAEDVVLAQEAVRA
                 (stage V sporulation)"                                      PSSIHETVYENDGDPITLLDQIADNSEEKWFDKIALKEAISDLEEREKLIYYLRYKD
                                                                            QTQSEVAERLGISQVVSRLEKKILKQIKVQMDHTDG"

                                                                    gene    complement(48177..48617)
                                                                            /gene="spoIIAB"
                                                                    CDS     complement(48177..48617)
                                                                            /gene="spoIIAB"
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                /function="binding to sigma-F (SpoIIAC) in the presence of
                ATP before septation; phosphorylation of SpoIIAA (stage II
                sporulation)"
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                /transl_table=11
                /product="anti-sigma factor (antagonist of sigma-F) and
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                /db_xref="SWISS-PROT:P10728"
                /translation="MKNEMHLEFSALSQNESFARVTVASFIAQLDPTMDELTEIKTVV
                SEAVTNAITHGYEENCEGKVYISVTLEDHVVYMTIRDEGLGITDLEEARQPLFTTKPE
                LERSGMGFTIMENFMDDVSIDSSPEMGTTIRLTKHLSKSKALCN"
gene            complement(48614..48967)
                /gene="spoIIAA"
CDS             complement(48614..48967)
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                /function="binding to SpoIIAB in the presence of ADP
                selectively in the forespore (stage II sporulation)"
                /codon_start=1
                /transl_table=11
                /product="anti-anti-sigma factor (antagonist of SpoIIAB)"
                /protein_id="CAB14279.1"
                /db_xref="GI:2634782"
                /db_xref="SWISS-PROT:P10727"
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                HIVLNLEDLSFMDSSGLGVILGRYKQIGGEMVVCAISPAVKRLFDMSGLFKIIRF
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gene            complement(49063..50232)
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CDS             complement(49063..50232)
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                /function="peptidoglycan biosynthesis"
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                /db_xref="SWISS-PROT:P38422"
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                LIKFYPGVDGVKTGYTGEAKYCLTASAKKGNMRAIAVVFGASTPKERNAQVTKMLDFA
                FSQYETHPLYKRNQTVAKVKVKKGKQKFIELTTSEPISILTKKGEDMNDVKKEIRMKD
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terminator      complement(50333..50362)
                /gene="pnp"
gene            complement(50333..51202)
                /gene="pnp"
CDS             complement(50387..51202)
                /gene="pnp"
                /EC_number="2.4.2.1"
                /function="cleavage of guanosine or inosine to respective
                bases and sugar-1-P molecules (purine nucleoside salvage)"
                /note="alternate gene name: yqkO"
                /codon_start=1
                /transl_table=11
                /product="purine nucleoside phosphorylase"
                /protein_id="CAB14281.1"
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                VEALIVTNAAGGVNTEFRAGDLMIITDHINFMGTNPLIGPNEADFGARFPDMSSAYDK
                DLSSLAEKIAKDLNIPIQKGVYTAVTGPSYETPAEVRFLRTMGSDAVGMSTVPEVIVA
                NHAGMRVLGISCISNAAGILDQPLSHDEVMEVTEKVKAGFLKLVKAIVAQYE"
gene            complement(51215..52399)
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CDS             complement(51215..52399)
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                /function="conversion of ribose-1-P/deoxyribose-1-P to
                ribose-5-P/deoxyribose-5-P (purine nucleoside salvage)"
                /note="alternate gene name: yqkN"
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                /transl_table=11
                /product="phosphodeoxyribomutase"
                /protein_id="CAB14282.1"
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                /db_xref="SWISS-PROT:P46353"
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                GLHMPNMAKLGLGLIEDIKGVEKTEHPLAYYGKLQEASNGKDTMTGHWEIMGLYIDKP
                FKVPEGFPDELLQELEKRSGRKIIGNKPASCTAILDELGQEHMETGALIVTSADSV
                LQIAAHEVVPLEELYRICETARELTLDPKYMVGRIIARPFVGEPGQFKRTPNRHDYA
                LKPFDRTVMNELKDCGLDVISIGKISDIYDGEGITSSRRTVSNMDGMDKVIDTLGEDF
                TGLSFANLVDFDALFGHRRDPEGYGRALEEFDARLPEVFKGMREDDLLIITADHGNDP
                IHHGTDHTREYVPILAYSKKHKKAQMLPLADTFADIGATIADNFQTNKPKYGKSFLSL
                LQ"
gene            complement(52543..53450)
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terminator      complement(52543..52560)
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CDS             complement(52560..53450)
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                KTERALPKVLALNEVERLDTPKLTSPFGYRDKAMLELLYATGIRVSEMIELKTADVH
                LSMGFIRCFGKGRKERIVPIGEAAASAIEEYMTKARGKLLKNNVSDALFLNHHGKQIS
                RQGFWKNLKKIALEAGIKKELTPHTLRHSFATHLLEDGADLRAVQEMLGHADISTTQI
                YTHVTKTRLKDVYKQFHPRA"
gene            complement(53771..54258)
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terminator      complement(53771..53791)
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CDS             complement(53809..54258)
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                /function="unknown"
                /note="similar to transcriptional regulator (Fur family)"
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                LLVKEKSPEIGLATVYRTLELLTELKVVDKINFGDGVSRYDLRKEGAAHFHHHLVCME
                FGAVDEIEGDLLEDVEEIIERDWKFKIKDHRLJTFHGICHRCNGKETE"
gene            complement(54371..55015)
                /gene="spoIIM"
CDS             complement(54371..55015)
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                /function="required for dissolution of the septal cell
                wall (stage II sporulation)"
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                MIFLKGIVVGFTVGFLSVLVNQGVSGFELSFSVSLPQNVLILPAYLIMGTCAIAFSLKLI
                RQLFVKRSLHDAPIQWFGRYAFVLIVFLALISSLFEAYLSPVLMEKLTSRLF"
gene            complement(55116..55331)
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CDS             complement(55116..55331)
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terminator

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CDS           /gene="yqkJ"
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              RSLAELGRVVTPGVADVCRLIEKEPEKASIYTTISNSVAIVTDGTAILGLGNIGSVAG
              MPVMEGKAALFDQLAGISGIPILLDYSDPEEIIKTVKHISPFGSGLLEDIGSPHCFE
              IEDRLKEELNIPVMHDDQHGTAVVTLAAAISACRSAGVDLKEAKVGQIGLGAAGVAIC
              RMFMAYGVNAVYGTDKSESAMNRLEQYGGQAVSSIEELMETCDIVIATTGVPGLIKPA
              FVRSGQVILALSNPKPEIEPEAALQAGAAYAADGRSVNNVLGFPGIFRGALNAKSTEI
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gene          /gene="yqkI"
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CDS           complement(56768..58174)
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              /function="unknown"
              /note="similar to Na+/H+ antiporter"
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              /db_xref="SWISS-PROT:P54571"
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              DLDKVEFLKSSLQNTFDIHIWMLIPAVLVLLAMKPSMPVIVIGALLGAIWAVVFQ
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              LKVIVSTFEKKLTSAGNVTLSTLIVAFLANIFGCAMYVSLILTPKIMEDSYDRLHLDR
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              EKLLKTMEDMHSVFKQKAQEFHSVIKMGRTHLQDAVPIRLGQEFEAYSRVLERDIKRI
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              SYDAFESINYPYIAFINEDGIEYNKQVTEPENDTFTVDTSLCTDVCLLKLHPGLKPEM
              FDALKSMYKGIVIESYGSGGVPFEGRDILSKYNELIESGIVVVITTQCLEEGEDMSIY
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gene          /gene="ansR"
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CDS           60958..61308
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gene          /gene="yqxK"
              complement(61317..62201)
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              GLDPLLGKYQTACEACGEPAVSGETACANCGKARFTKGVSDRLRELSDQLEVRVPRP
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gene          /gene="yqkG"
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              KKSNIVSIMMQFSLFDRRPEEWLPLLEEHQISVARGPVAKGLLTEKPLDQASESMKQ
              NGYLSYSFEELTNARKAMEEVAPDLSMTEKSLQYLLAQPAVASVITGASKIEQLRENI
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terminator    64224..64245
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gene            complement(64247..64471)
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CDS             complement(64247..64471)
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terminator      65555..65579
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                EQMKANGYTPKGENGIAGRRYFQKGGNKRIHHVHMYEQGNPAIERHLLFRDYLRAHPN
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CDS          complement(72518..73399)
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CDS          77120..77956
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gene            83125..84635
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terminator          complement(89613..89636)
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gene                complement(90781..92301)
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CDS                 complement(90781..92301)
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CDS                 complement(93504..94472)
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                    AVIFAEIERYLLTGEQDWSGKEIPETHQLITEAKNLAYRDVQNHILRYENLHYHYFKM
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gene                complement(94543..95265)
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CDS                 complement(94543..95265)
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                    NPKEFFMSPPKSKRAQDFLEKIL"
gene                complement(95258..95917)
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CDS                 complement(95258..95917)
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terminator          complement(95968..95989)
CDS                 complement(95998..96765)
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                    /function="unknown"
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                    FKTEDRNRISDLIVQEIKSDRFDAAIIEDIVAEGYFKSNDDLQGFVIPDAKAEEAGSAI
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gene                complement(97001..97471)
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gene          97634..98527
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CDS           97634..98527
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gene          98628..99797
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CDS           98628..99797
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              /transl_table=11
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              PFFFAAFALLAAILSILTLREPERNPENQEIKGQKTGFKRIFAPMYFIAFLILISS
              FGLASFESLFALFVDHKFGFTASDIAIMITGGAIVGAITQVVLFDRFTRWFGEIHLIR
              YSLILSTSLVFLLTTVHSYVAILLVTVTVFVGFDLMRPAVTYLSKIAGNEQGFAGGM
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gene          99870..100709
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CDS           99870..100709
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              IAE"
terminator    complement(100725..100759)
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gene          complement(100725..102045)
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CDS           complement(100771..102045)
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              /EC_number="2.3.1.-"
              /note="alternate gene name: bfmB2"

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gene          complement(102068..103051)
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CDS           complement(102068..103051)
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              /EC_number="1.2.4.4"
              /note="alternate gene name: bfmB1b"
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gene          complement(103065..104057)
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gene          complement(104131..105504)
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CDS           complement(104131..105504)
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              LEVDGKSVLTSDEALQMEELPQSIIVGGVGIEWASMLHDFGVKVTVIEYADRILP
              TEDLEISKEMESLLKKGIQFITGAKVLPDTMKTSDDISIQAEKDGETVTYSAEKML
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              GIIAVEHFAGLNPHPLDPTLVPKCIYSSPEAASVGLTEDEAKANGHNVKIGKFPFMAI
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gene          complement(105525..106616)
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               ERAGTVPAGDLVDLCFSGEYTKEEIMKKLVGTGGLLGYLGTNDAVKVEQMIQGGDEKA
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gene           /gene="yqiT"
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Left column:

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CDS         complement(114782..115918)
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            /EC_number="1.3.99.-"
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            CVYEGVRTEAIDEVMKLGMNHPMGPLALADFIGLDTCLSIMEVLHSGLGDSKYRPCPL
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gene        complement(116729..118011)
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terminator  complement(116729..116742)
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            /protein_id="CAB14348.1"
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            RAQDADILVAGGMESMSNIPYAVPGRWGARAGDGELRDLMVYDGLTCAFDEVHMAVH
            GNTAAKEYAISRREQDEWALRSHARAKAADEGKFQDEIVPVNWIGRKGKPNVVDKDE
            AIRRDTSLDQLAKLAPIYASDGSITAGNAPGVNDGAGAFVLMSEEKAAELGKRPLATI
            LGFSTTGMPAHELAAAPGFAINKLLKKNGLTVQDIDLFEVNEAFASVVLTCEKIVGFD
            LEKVNVNGGAIALGHPIGASGARILMTLVYELKRRGGLGVAAICSGAAQGDAVLVQV
            H"

gene        complement(118108..118868)
            /gene="yqiK"
terminator  complement(118108..118126)
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CDS         complement(118149..118868)
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            /function="unknown"
            /note="similar to glycerophosphodiester phosphodiesterase"
            /codon_start=1
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Right column:

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            VLTSDVLYQADRYIASIPASGYHPKINSPGVTDEVLKKMRNGLIKVRPYTVNRPEDMK
            RLIEAGADRMFTDFPERLRHC"
            complement(118947..119567)
            /gene="yqiI"
CDS         complement(118947..119567)
            /gene="yqiI"
            /function="unknown"
            /note="alternate gene name: yqiI
            similar to N-acetylmuramoyl-L-alanine amidase"
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            /transl_table=11
            /protein_id="CAB14350.1"
            /db_xref="GI:2634853"
            /db_xref="SPTREMBL:O32017"
            /translation="MRMLWRSLALCGLALTLAPCAQAEPIEGKTVYIDAGHGGEDSG
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            SIHVNSGVASASGTETYFQSDYEGENSRRLASDIQSQLVSSLQTRDRGVKESDFYVIT
            YSQMPSVLAELGFITNSSDADKLGSEEYQQKAADAIVNGIDSYDQ"

gene        complement(119582..119875)
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CDS         complement(119582..119875)
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            /function="unknown"
            /note="alternate gene name: yzpA
            similar to lipoprotein"
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gene        120407..121557
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CDS         120407..121525
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            /function="unknown"
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            /db_xref="SWISS-PROT:P54524"
            /translation="MNPKYKPLFEPFTFKSGVTINNRIAVAPMTHYASNEDGTISEAE
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            VQIHGGIECPSELVPQODVVGPSDVFDNGKQIARALTEEEVENIVKAFGEATRRAIE
            AGPDGVEIHGANGYLIQQFYSPKTNQRTDRWGGSDEKRLAFPLAIVDEVKKAASEHAK
            GAFLVGYRLSPEEPETGLTMTETYTLVDALGDKELDYLHISLMDVNSKARRGADPTR
            TRMDLLNERVGNKVPLIAVGSIHSADDALAVIENGIPLVAMGREILVDPNWTVKVKEG
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terminator  121534..121557
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gene        complement(122041..122844)
            /gene="spo0A"
CDS         complement(122041..122844)
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            /function="central role in the initiation of sporulation
            (negative regulation of abrB, kinA, kinC, spo0A; positive
            regulation of spoIIA, spoIIE, spoIIG) (stage 0
            sporulation)"
            /note="alternate gene name: spo0C, spo0G, spoIIL, sof-1"
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            SYFILKPFDMENLVGHIRQVSGNASSVTHRAPSSQSSIIRSSQPEPKKKNLDASITSI
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gene

terminator

CDS
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          complement(123120..124397)
          /gene="spoIVB"
          /function="intercompartmental signalling of pro-sigma-K
          processing/activation in the mother-cell; essential for
          spore cortex and coat formation (stage IV sporulation)"
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          TMFYEPKIKKYGALGHVISDMDFKKPIVVENGEIVKSTVTSIEKGTGNPGEKLARF
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          /gene="recN"
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          /db_xref="SWISS-PROT:P17894"
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          KSVCRVNGKLVTIASLREIGRLLLDIHGQHDNQLLMEDENHLQLLDKFAGAEVESALK
          TYQEGYQRYVIASLELQLSESEQEMAHCLDLIIOFQLEEIESAKLELNEDEQLQEERQ
          QISNFEKIYESLQNAYNALRSEQGGLDWVGMASAQLEDISDINEPLKKMSESVSNSYY
          LLEDATFOMRNMLEDEFDPERLNYIETRLNEIKQLKRKYGATVEDILEYASKIEEEI
          DQIENRDSHADSLKKELDSVGDKVDAVEAANVSQIRKTWAKKLADEIHRELKSLYMEKS
          TFDTEFKVRTASRNEEAPLVNGQPVQLTEQGIDLVKFLISTNTGEPLKSLSKVASGGE
          LSRVMLAIKSIFSSQODVTSIIFDEVDTGVSGRVAQAIAEKIHKVSIGSQVLCITHLP
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          KQADQVKTG"
          complement(126339..126788)
          /gene="ahrC"
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          /gene="ahrC"
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          and positive regulation of arginine catabolism (roc
          operons)"
          /codon_start=1
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          /product="transcriptional regulator"
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gene

CDS




gene

CDS



gene

CDS



gene

CDS
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          NGAKQSYAVDVGYNQLAWKLRQDERVVMERTNFRYATPADFTKGMPEFATIDVSFIS
          LRLILPVLRTLLVPGSDCMALVKPQFEAGRESVGKKGIVRDPKVHADVLKRMISFSAA
          EGYICKGLSFSPITGDGNIEFLLQFALAGRGTGRPGTAGRRDHARCRRST"
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          SESEHDVWETGHSSTSLSGAMGMAAARDIKGTDEYIIPIIGDGALTGGMALEALNHIG
          DEKKMIVILNDNEMSIAPNVGAIHSMLGRLRTAGKYQWVKDELEYLFKKIPAVGKL
          AATAERVKDSLKYMLVSGMFFEELGFTYLGPVDGHSYHELIENLQYAKKTKGPVLLHV
          ITKKGKYKPAETDTIGTWHGTGPYKINTGDFVEPKAAAPSWSGLVSGTVQRMAREDG
          RIVAITPAMPVGSKLEGFAKEFPDRMFDVGIAEQHAATMAAAAMOGMKPFLAIYSTF
          LQRAYDQVVHDICRQNANVFIGIDRAGLVGADGETHQGVFDIAFMRHIPNMVLMMPKD
          ENEGQHMVHTALSYDEGPIAMRFPRGNGLGVKMDEQLKTIPIGTWEVLRPGNDAVILT
          FGTTIEMAIEAAEELQKEGLSVRVVNARFIKPIDEKMMKSILKEGLPILTIEEAVLEG
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          /function="unknown"
          /note="similar to geranyltransferase"
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          /db_xref="SWISS-PROT:P54383"
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          HKVFGEATAVLAGDGLLTESFKLITSHVSDEVSAEKRLRLVNELISAAGTEGMVGGQV
          ADMEAGNRQVTLEEELESIHERKTSKLLGFCVIAGAILADAPEEDIETLRTFSSHIGIG
          FQIRDDILDLEGSEEKIGKRVGSDTTNDKSTYPSLLSLSLEGAKHKLDVHIKEAND"
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          /function="unknown"
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          /db_xref="SWISS-PROT:P54522"
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          /function="unknown"
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                    IVARAIFASNIVISAVGHEFTISDFVADIRAATPTGAAEIAVPHTTDLIERTKTA
                    EVRMTRAMQQHLGQEKGRIQTLQSSYAFRFPKRLYAQKEQQFDLAYQQFQAQLTALLD
                    RKSRQLERETYRLEALHPHEQLKQARTRYQEQTNQLRKNMNIQMKQLHSQFQTVLGKL
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gene                complement(132419. .133270)
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CDS                 complement(132419. .133270)
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                    /EC_number="3.5.4.9"
                    /function="purines and amino acids biosynthesis"
                    /note="alternate gene name: yqiA;
                    methylenetetrahydrofolate dehydrogenase"
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                    VVVVGRSNIVGKPVGQLLNENATVTYCHSRTENITEHTKKADILVVAVGRANFISAD
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gene                complement(133282. .133677)
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CDS                 complement(133282. .133677)
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gene                complement(133902. .134348)
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terminator          complement(133902. .133924)
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CDS                 complement(133941. .134348)
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gene                complement(134369. .135721)
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gene                complement(135733. .136212)
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CDS                 complement(135733. .136212)
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gene                complement(136334. .137024)
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terminator          complement(136334. .136352)
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CDS                 complement(136368. .137024)
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                    (stage III sporulation)"
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gene                complement(137025. .137714)
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gene                complement(137707. .138327)
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CDS                 complement(137707. .138327)
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CDS          complement(138324..139541)
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             NYATEAIQTMTSFLALIPLLLALLASSGGAVSAAFFHPVILEFLMNTSGLLIQNIVMP
             LIFLSAILSIVSTMTEQYKVTQLANLLRNIAIGALAVFLTIFLGVISVQGASAAVTDG
             ITLRTAKFITGNFIPVLGRMFTDATDTVISASLLLKNTVGILGVAILCIAAFPAIKV
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             (stage III sporulation)"
             /codon_start=1
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             /db_xref="GI:2634875"
             /db_xref="SWISS-PROT:P49780"
             /translation="MGVDVNVIFQIAGVGVIVVAFLHTILDQMGKKEYAQWVTLLGFIY
             ILFMVATIVDDLFKKIKAVFLFQG"
gene         complement(140197..140712)
             /gene="spoIIIAB"
CDS          complement(140197..140712)
             /gene="spoIIIAB"
             /function="mutants block sporulation after engulfment
             (stage III sporulation)"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14373.1"
             /db_xref="GI:2634876"
             /db_xref="SWISS-PROT:Q01368"
             /translation="MLKLLGAVFIVVATTWTGFEMAKIYTERPRQIRQLRAALQSLEA
             EIMYGHTPLHTASQQIAKQLAQPVSTLFSAFSDQLDKGSDSAKTAWEQSLKKYWDTLS
             LKKSEYEVLKQFGETLGIHDRISQQKHIKLALTHLEASEADAEQAQAKNEKMIKSLGF
             LAGLLLILLM"
gene         complement(140706..141629)
             /gene="spoIIIAA"
CDS          complement(140706..141629)
             /gene="spoIIIAA"
             /function="mutants block sporulation after engulfment
             (stage III sporulation)"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14374.1"
             /db_xref="GI:2634877"
             /db_xref="SWISS-PROT:Q01367"
             /translation="MNEIAEVLPESMKNALSEIPEQQWLEIEEVRIRINRPVELIRRG
             QPVYLSYAGTAEDAHLILSRLSNYSMYTLEELKKGYVTIRGGHRVGLAGRVITENGG
             VKGLRDIASFNIRIARQKIGIAEPLLPYLYQNSWLNTLIIGPPQTGKTTLLRDLARLS
             STGKKNMLPVKTGIVDERSEIAGCLRGRIVPQHQFGQRIDVLDACPKAEGLMMIRSMSP
             EVMIVDEIGRMEDTDALLEALHAGVSVIVSAHGWSISDLMKRPSLKRLWEERAFDRYL
             ELSRAKGPGTVSQIYDKDGNVLSRTTGVKTC"
gene         complement(141705..141986)
             /gene="yqhV"
CDS          complement(141705..141986)
             /gene="yqhV"
             /function="unknown"
             /note="alternate gene name: yqgE"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14375.1"
             /db_xref="GI:2634878"
             /translation="MKFLLGNINSTVLTMAGLRVLSSMIELTAATVMLVTNDVRKAVV
             VNSILAIVGPLIFIITMTVGIYQIAGQLSYAKLLIFTGVVLILAGVHK"
gene         complement(142093..142688)
             /gene="efp"
terminator   complement(142093..142116)
             /gene="efp"
CDS          complement(142131..142688)
             /gene="efp"
             /note="alternate gene name: yqhU, yqgF"
             /codon_start=1
             /transl_table=11
             /product="elongation factor P"
             /protein_id="CAB14376.1"
             /db_xref="GI:2634879"
             /db_xref="SWISS-PROT:P49778"
             /translation="MISVNDFRTGLTIDVDGGIWRVVDFQHVKPGKGAAFVRSKLRNL
             RTGAIQEKTPRAGEKVAKAQIETKTMQYLYANGDQHVFMDTSSYEQLELSATQIEEEL
             KYLLENMSVHIMMYQDETLGIELPNTVELKVVETEPGIKGDTASGTKPAKTETGLVV
             NVPFFVNEGDTLVVNTSDGSYVSRA"
gene         complement(142713..143774)
             /gene="yqhT"
CDS          complement(142713..143774)
             /gene="yqhT"
             /function="unknown"
             /note="similar to Xaa-Pro dipeptidase"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14377.1"
             /db_xref="GI:2634880"
             /db_xref="SWISS-PROT:P54518"
             /translation="MKLEKLRNLFGQLGIDGMLITSNTNVRYMTGFTGSAGLAVISGD
             KAAFITDFRYTEQAKVQVKGFEIIEHGGSLIQTTADTVESFGIKRLGFEONSMTYGTY
             ASYSAVISDAELVPVAESVERLRLIKSSEEIKILEEAAKIADDAFRHILTFMKPGISE
             IAVANELEFYMRSQGADSSSFPDMIVASGLRSSLPHGVASDKLIESGDLVTLDFGAYYK
             GYCSDITRTVAVGQPSDQLKEIYQVVFDAQALGVAHIKPGMTGKEADALTRDHIAAKG
             YGDYFGHSTGHGLGMEVHESPGLSVRSSAILEPGMVVTVEPGIYIPETGGVRIEDDIV
             ITENGNRTITHSPKELIIL"
gene         complement(143771..144217)
             /gene="yqhS"
CDS          complement(143771..144217)
             /gene="yqhS"
             /function="unknown"
             /note="similar to 3-dehydroquinate dehydratase"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14378.1"
             /db_xref="GI:2634881"
             /db_xref="SWISS-PROT:P54517"
             /translation="MPHFLILNGPNVNRLGSREPEVFGRQTLDIETDLFQFAEALHI
             QLTFFQSNHEGDLIDAIHEAEEQYSGIVLNPGALSHYSYAIRDAVSSISLPVVEVHLS
             NLYAREFRHQSVIAPVAKQIVGLGAEGYKLAVRYLLSQQGESR"
gene         complement(144304..144840)
             /gene="yqhR"
             /function="unknown"
             /codon_start=1
             /transl_table=11
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               /protein_id="CAB14379.1"
               /db_xref="GI:2634882"
               /db_xref="SWISS-PROT:P54516"
               /translation="MMTSEKDTEQNEELNEKQKPPVSMAGRVAATGFCGGVLWSFVAY
               IAYLFHFSEISPNMLQPFVLGEWKKHGLGTVISILIGVISIGAAFLYFLLLKRLKT
               MWPGILYGLVLWLLVFFVFVNPIFPDVRTVTELTSDTIITTICIYLLYGLFVGYSISFE
               YNELNSEKLARALGMHRE"
gene    145067. .146023
CDS     145067. .146023
               /gene="yqhQ"
               /function="unknown"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14380.1"
               /db_xref="GI:2634883"
               /db_xref="SWISS-PROT:P54515"
               /translation="MSKHKVPPAYGGQAVVEGVMFGGKHHYVTAIRRTDGSIDFFKLP
               RKHNPKLNIVKKIPLRGIAAIIEASANGTKHLNFSSERYGLDPSEDETLEQEEKKSS
               GLSMYLSLAVIGVLSFLFSKFVFTLVPVFLAELTRPIFSLNTAQIAIESLFKLILLLG
               YIYFLSMTPLIKRVFRQYHGAEHKVINCYEQNLPITVENVQNQSRLHYRCGSSFILFTI
               IVGMFVYLLVPTDPWLRVIDRVALIPVVLGISFEVLQLTNKVRDIRGLKLLGYPGLW
               LQLLTTKEPKDEQVEVAIFSFNELLRLEALSEQNQKPSHNVI"
gene    146063. .146458
CDS     146063. .146458
               /gene="yqhP"
               /function="unknown"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14381.1"
               /db_xref="GI:2634884"
               /db_xref="SWISS-PROT:P54514"
               /translation="MNHRVQPIIAVLIALGAFGFLYVLVTNPGEMAKMAVTVIVAGII
               IYFIVKYVMNRNAGSEGAAFKKAAKQSRRRMKEQKAKHRAGHKGRVSHLRSVPSASKP
               KPMILKKKSQTLQTVIEGKKNKKKNRALF"
gene    complement(146455. .147330)
               /gene="yqhO"
CDS     complement(146455. .147330)
               /gene="yqhO"
               /function="unknown"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14382.1"
               /db_xref="GI:2634885"
               /db_xref="SWISS-PROT:P54513"
               /translation="MYIDGVFSGGGVKGIALAGAYEVLEEKGFRFKRVAGTSAGAIIA
               AFIASGYTSKEIHALIEEVDGEKLIQDRYSFLPLKMLQWVSIYWRLGLYKGDTIEKWI
               ADLLRAKGIRVFDQKGSLRLIASDLTNGTMIVLPDDLARYGLNPDMFPVARAVRMS
               CSIPYFFEPIKLKTDTGTATVVDGGVLSNFPIWLFSKERKRPVIGVTLAPRERERPKK
               NIRNAFELFGALFETMKDAHDARHIASRYEQNIIFLPVDDVMATDFHLTQQKKLALIE
               LGKRNTELFLKQWTY"
gene    146499. .146517
               /gene="yqhN"
terminator  146499. .146517
               /gene="yqhN"
gene    complement(147431. .147884)
               /gene="yqhN"
terminator  complement(147431. .147452)
               /gene="yqhN"
CDS     complement(147456. .147884)
               /gene="yqhN"
               /function="unknown"
               /note="similar to transcriptional regulator"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14383.1"
               /db_xref="GI:2634886"
               /db_xref="SWISS-PROT:P54512"
               /translation="MTTPSMEDYIEQIYMLIEEKGYARVSDIAEALAVHPSSVTKMVQ
               KLDKDEYLIYEKYRGLVLTSKGKLIGKRLVYRHELLDQFLRIIGVDEEKIYNDVEGIE
               HHLSWNSIDRIGDLVQYFEEDDARKKDLKSIQKKTEHHNQ"
gene    complement(147984. .148820)
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CDS     complement(147984. .148820)
               /gene="yqhM"
               /function="unknown"
               /note="similar to hypothetical proteins from B. subtilis"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14384.1"
               /db_xref="GI:2634887"
               /db_xref="SPTREMBL:O32018"
               /translation="MQKETWRFIDSGNASPAFNMALDEALLYWHSEKKIPPVIRFYGW
               NPATLSVGYFQNIKKEINFEEAVHKYNLGFVVRPTGGRGVLHDQELTYSIVSEEHPEM
               PATVTEAYRVISEGILQGFRNLGLDAYFAIPRTEKEKESLKNPRSSVCFDAPSWYELV
               VEGRKVAGSAQTRQKGVILQHGSILLDLDEDKLFDLFLYPSERVRERMQRNFKNKAVA
               INELIEKRVTMDEARKAFKEGFETGLNIHLEPYELSQEELDFVHHLAETKYASDEWNY
               KR"
gene    149011. .149418
               /gene="yqhL"
CDS     149011. .149391
               /gene="yqhL"
               /function="unknown"
               /note="similar to hypothetical proteins"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14385.1"
               /db_xref="GI:2634888"
               /db_xref="SWISS-PROT:P54510"
               /translation="MSNMIVLIIFPAFIYMIASYVVQQRIMKTLTEEEFRAGYRKAQ
               LIDVREPNEFEGGHILGARNIPLSQLKQRKNEIRTDKPVYLYCQNSVRSGRAAQTLRK
               NGCTEIYNLKGGFKKWGGKIKAKK"
terminator  149398. .149418
               /gene="yqhL"
gene    complement(149426. .150892)
               /gene="yqhK"
CDS     complement(149426. .150892)
               /gene="yqhK"
               /function="unknown"
               /note="similar to glycine dehydrogenase"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14386.1"
               /db_xref="GI:2634889"
               /db_xref="SWISS-PROT:P54377"
               /translation="MSNQDQALIFELSREGRIGYSLPELDVPEIELGDLLSDTYIRDE
               DAALPEVSELDIMRHYTALSKRNGHQGFYPLGSCTMKYNPKINEKIARIPGFAAIH
               PLQDEDTVQGALELLYDLSKHLEEITGMDEVTLQPAAGAHGEWTGLMMIRAYHEARGD
               FKRTKVIVPDSAHGTNPASATVAGFETVTVKSNEKGLVDLEDLKRAVNEETAALMLTN
               PNTLGLFEEQTEMAEIVHQAGGKLYNQAGANLNAVLSKARPGDMGFDVVHLNLHKTFT
               GPHGGGGPSGPVGVKQDLIPYLPKPVVLVKSGRFTFDYDRPHAIGRVKPYYGNFGIN
               VRAYTYIRSMGPDGLKAVTENAVLNANYMMRKLAPYDLPFDRHCKHEFVLSGKRQKK
               LGVRTLDIAKRLLDFGYHPPTIYFPLNVEECIMIEPTETESKETLDAFIDAMIQIAKE
               AEENPELVQEAPHTIVKRMDETKAARHPVLRYEAEER"
gene    complement(150885. .152231)
               /gene="yqhJ"
CDS     complement(150885. .152231)
               /gene="yqhJ"
               /function="unknown"
               /note="similar to glycine dehydrogenase"
               /codon_start=1
               /transl_table=11
               /protein_id="CAB14387.1"
               /db_xref="GI:2634890"
               /db_xref="SWISS-PROT:P54376"
               /translation="MKHRYLPATEKDKQEMLATIGVSSIDDLFADIPENVKKKEHQI
               KKAKSETELTRELTKLASKNRDTVQTASFLGAGVYDHYQPVIVDHVISRSEFYTAYTP
               YQPEISOGELQAIFEFQTMICELTGMDIANSSMYDGTALAEAAMLASGHTKKKIVV
               SKTVHPESREVLKTYAKQYIDVVEVPAADGVTDLDALRQTVCENTAAVIVQPNFFG
               RIEPLKDIEPIAHQGKSMFIVSANPLALGLLTPPGKFQSDIVVGDAHRFGIPSAYGGP
               HCGFFAVTKKLMRKVPGRLVGQTEDENGKRGFVLTLQAREQHIRRDKATSNICSNQAL
               NALAASVAMTALGKNGVKIADYDIARQNLLKANYAKQEAKKAGLTVMFDGPMFNEFVIKLDE
               PVRAVNKRLLAKGMIGGYDLGLTYPELDCHMLIAVTELRTKEEIDALIQELGDRHE"
gene    complement(152261. .153349)
               /gene="yqhI"
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CDS          complement(152261..153349)
             /gene="yqhI"
             /function="unknown"
             /note="similar to aminomethyltransferase"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14388.1"
             /db_xref="GI:2634891"
             /db_xref="SWISS-PROT:P54378"
             /translation="MLKRTPLFDLYKEYGGKTIDFGGWELPVQFSSIKKEHEAVRTAA
             GLFDVSHMGEVEVSGNDSLSFLQRLMTNDVSALTPGRAQYTAMCYPDGGTVDDLLIYQ
             KGENRLLVINASNIDKDLAWMKEHAAGDVQIDNQSDQIALLAVGGPKAEAILKNLTD
             ADVSALKPFAFIDEADISGRKALISRTGYTGEDGYEIYCRSDDAMHIWKKIIDAGDAY
             GLIPCGLGARDTLRFEANVPLYGQELTRDITPIEAGIGFAVKHKKESDFFGKSVLSEQ
             KENGAKRKLVGLEMIEKGIPRHGYEVFQNGKSVGKVTTGTQSPTLGKNVGLALIDSET
             SEIGTVVDVEIRKKLVKAKVVKTPFYKR"

gene         153791..155464
             /gene="yqhH"

CDS          153791..155464
             /gene="yqhH"
             /function="unknown"
             /note="similar to SNF2 helicase"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14389.1"
             /db_xref="GI:2634892"
             /db_xref="SWISS-PROT:P54509"
             /translation="MNTEMIYDAKWPEEFAERLKNDGPANWELYKLSAEIQKTLAIP
             EFEGLRAPLYLPSFTPLPHQLEVAQKVEKMNGKAILADEVGLGKTVEAGLILKEYMI
             RGLAKKILILVPASLVSQWVKELQEKFLIPAVEQKKSYVWEQCDIVVSSIDTAKRSPH
             REIVLSIPYDLVIIDEAHKLKNSKTKNYFEFVRNLVKKYCLLLTATPIQNRIEEIFNLV
             SLLKPGHLGSQNHFQEEFAKKKSSLEAHEHLKDLVNKVMIRNRRHDTGLNWKQRHVET
             VPIQFSPSEQALYDEISRLKDSINKPASMFSIMTLQRECCSSREAVYMTLKKMLDQKE
             KQAPAIDEDTISVLIDRINQVTQNSKALQVVDLIKKIDDKVIIFTEYRATQIYLQWFL
             QQNGISSVPFRGGFKRGKKDWMKDLFRGKIQVLIATEAGGEGINLQFCNHMINYDLPW
             NPMRLEQRIGRIHRLGQERDVHIYNMATKHTVEEHILKLLYFEKVVGELDDIL
             TKIQVNNFEEHLHDILYHSATEEEMKIKMDNLTSFLSYKKQLPAEKRGS"

gene         155485..156279
             /gene="yqhG"

CDS          155485..156279
             /gene="yqhG"
             /function="unknown"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14390.1"
             /db_xref="GI:2634893"
             /db_xref="SWISS-PROT:P54508"
             /translation="MRQQEVHDFLLRFFQANSCQIVDQGLGYMTVQLTVEMDKQIMNR
             PFYWHWREKTGGDPNPMKITFITDKENAPKDLDGEFIYFGAPRLFQIFKAVKQNGRFT
             RMYEKIESAGAKVPLQPWLGINVFYQPWLGINVISYQSDMKKDKLLSLGLHLVSGTIIEDFQSKLTQ
             FSLTSQICDYCFTISPMIKPESGLKRMENYISKSSAMQEPSDWAEQAVNRRWKNDMTLLD
             KFYEHIEEKPEEYHLEKQALKTLYQPKISVEIENGGLFYLQNNISS"

gene         156462..156635
             /gene="sinI"

CDS          156462..156635
             /gene="sinI"
             /function="prevents SinR from binding to its target
             sequence on aprE"
             /codon_start=1
             /transl_table=11
             /product="antagonist of SinR"
             /protein_id="CAB14391.1"
             /db_xref="GI:2634894"
             /translation="MKNAKQEHFELDQEWVELMVEAKEANISPEEIRKYLLLNKKSAH
             PGPAARSHTVNPF"

gene         156669..157030
             /gene="sinR"

CDS          156669..157004
             /gene="sinR"
             /function="regulation of post-exponential-phase responses
             genes (positive regulation of comK; negative regulation of
             aprE, kinB, sigD, spo0A, spoIIA, spoIIE, spoIIG, spoIIG)"
             /note="alternate gene name: sin, flaD"
             /codon_start=1
             /transl_table=11
             /product="transcriptional regulator"
             /protein_id="CAB14392.1"
             /db_xref="GI:2634895"
             /db_xref="SWISS-PROT:P06533"
             /translation="MIQRIKQYRKEKGYSLSELAEKAGVAKSYLSSIERNLQTNPSI
             QFLEKVSAVLDVSVHTLLDEKHETEYDGQLDSEWEKLVRDAMTSGVSKKQFREFLDYQ
             KWRKSQKEE"

             156995..157030
             /gene="sinR"

gene         complement(157048..157882)
             /gene="cotN"

terminator   complement(157048..157081)
             /gene="cotN"

CDS          complement(157097..157882)
             /gene="cotN"
             /note="alternate gene name: yqhF"
             /codon_start=1
             /transl_table=11
             /product="spore coat-associated protein"
             /protein_id="CAB14393.1"
             /db_xref="GI:2634896"
             /translation="MGMKKLSLGVASAALGLALVGGTWAAFNDIKSKDATFASGTL
             DLSAKPNSASVNLSNLKPGDKLTKDFQFENNGSLAIKEVLMALNYGDFKANGGSNTSP
             EDFLSQPEVTLLTVGKEGGNGTPKNIILDDANLKDLYLMSAKNDAAAAEKIKKQIDPK
             FLNASGKVNVATIDGKTAPEYDGVKTPVTPTDFDQVQMEIQFKDDKTKDEKGLMVQNKYQ
             GNSIKLQFSFEATQWNGLTIKKDHTDKDGYVKENEKAHSEDKN"

gene         complement(157946..158518)
             /gene="sipW"

CDS          complement(157946..158518)
             /gene="sipW"
             /EC_number="3.4.21.89"
             /note="alternate gene name: yqhE"
             /codon_start=1
             /transl_table=11
             /product="type I signal peptidase"
             /protein_id="CAB14394.1"
             /db_xref="SWISS-PROT:P54506"
             /translation="MKLISNILYVIIFTLIIVLIVVISTRSSGGEPAVFGYTLKSVL
             SGSMEPFNTGSLILVKEITDVKELQKGDVITFMQDANTAVTHRIVDITKQGDHLLFK
             TKGDNNAAADSAPVSDENVRAQYTGFQLPYAGYMLHFASQPIGTAVLLIVPGVMLLVY
             AFVTISSAIREIERKTKALETDTKDSTMST"

gene         complement(158502..159263)
             /gene="yqxM"

CDS          complement(158502..159263)
             /gene="yqxM"
             /function="unknown"
             /note="alternate gene name: yqhD"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14395.1"
             /db_xref="GI:2634898"
             /db_xref="SWISS-PROT:P40949"
             /translation="MFRLFHNQQKAKTKLKVLLIFQLSVIFSLTAAICLQFSDDTSAA
             FHDIETFDVSLQTCKDFQHTDKNCHYDKRWDQSDLHISDQTDKGTVCSPFALFAVLE
             NTGEKLKKSKKWELHKLENARKPLKDGNVIEKGFVSNQIGDSLYKIETKKKKMKPGIY
             AFKVKPAGYPANGSTFEWSEPMRLAKCDEKPTVPKKETKSDVKKENETQKDIPET
             MKEETSQEAVTKEKETQSDQKESGEEDEKSNEADQ"

             159535..159861
             /gene="yqzG"

gene         159535..159861
             /gene="yqzG"
             /function="unknown"
             /codon_start=1
             /transl_table=11
             /protein_id="CAB14396.1"
             /db_xref="GI:2634899"
             /db_xref="SPTREMBL:O32019"
             /translation="MMIKQCVICLLSLLVFGTTAAHAEETPLVTARHMSKWEEIAVKEA
             KKRYPLAQVLFKQKVWDRKRKDEAVKQYHLTLREGSKEFGVFTISFDPYSQKVNKIA
             ILEEYQ"
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gene    complement(159844..160083)
        /gene="yqzE"
CDS     complement(159844..160083)
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        /function="unknown"
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        /transl_table=11
        /protein_id="CAB14397.1"
        /db_xref="GI:2634900"
        /db_xref="SPTREMBL:O32020"
        /translation="MKTNDYVKYMTQQFVKYIDTPRDERKDRKEVRKETKTPVSQQWF
        GILPYGFRLLAETEKITANKRIRSFKKWRTLLIFF"
gene    complement(160154..160528)
        /gene="comGG"
CDS     complement(160154..160528)
        /gene="comGG"
        /function="competence"
        /codon_start=1
        /transl_table=11
        /product="probably part of the DNA transport machinery"
        /protein_id="CAB14398.1"
        /db_xref="GI:2634901"
        /db_xref="SWISS-PROT:P25959"
        /translation="MYRTRGFIYPAVLFVSALVLLIVNFVAAQYISRCMFEKETKELY
        IGENLLQNGVLLSIRHVLEERKGQESTQQFLYGRVSYIHDTSIKEQKEINLRVSTDS
        GTERTAQIVFDQKQKKLLRWTE"
gene    complement(160529..160912)
        /gene="comGF"
CDS     complement(160529..160912)
        /gene="comGF"
        /function="competence"
        /codon_start=1
        /transl_table=11
        /product="probably part of the DNA transport machinery"
        /protein_id="CAB14399.1"
        /db_xref="GI:2634902"
        /db_xref="SPTREMBL:O32021"
        /translation="MLISGSLAAIIHLFLSRQQEHDGFTQQEWMISIEQMMNECKESQ
        AVKTAEHGSVLICTNLSGQDIRFDIYHSMIRKRVDGKGHVPILDHITAMKADIENGVV
        LLKIESEDQKVYQTAFPVYSYLGGG"
gene    complement(160938..161285)
        /gene="comGE"
CDS     complement(160938..161285)
        /gene="comGE"
        /function="competence"
        /codon_start=1
        /transl_table=11
        /product="probably part of the DNA transport machinery"
        /protein_id="CAB14400.1"
        /db_xref="GI:2634903"
        /db_xref="SWISS-PROT:P25957"
        /translation="MWRENKGFSTIETMSALSLWLFVLLTVVPLWDKLMADEKMAESR
        EIGYQMMNESISKYMSGEGAASKTITKNNHIYAMKWEEEGEYQNVCIKAAAYKEKSF
        CLSILQTEWLHAS"
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gene    complement(162000..162971)
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CDS     complement(162000..162971)
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CDS     complement(164506..165459)
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gene    165602..166930
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CDS     165602..166930
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terminator   168910..168934
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CDS          complement(171377..172507)
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gene         complement(172554..174506)
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terminator   complement(172554..172582)
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CDS          complement(172590..174506)
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                     SLTEIENYVTANAKDANKRLFGAAKGRNVILVSLESTQSFVINEKLNGEEITPFLNDF
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          AGFVISRLENNTGYTVIFSLSLSLFALAVMSFFLKRRESKGRFMLSKVFGERHSNMN
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gene         complement(195937..195962)
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gene
　
CDS

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ORIGIN
Z99116   Length: 218470   September 24, 2001 09:21   Type: N   Check: 4068   ..

Initial Score   =     110   Optimized Score   =     317   Significance   =   -0.63
Residue Identity =   51%   Matches           =     380   Mismatches     =     253
Gaps            =     98   Conservative Substitutions   =       0
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                                                                  ||  |||  |||
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                20              30              40              50              60              70
           --TAACAT--CCCGGCCATTCC------CCGTTTGCCAGCGAGTCCAGCGTA--TAGCTGCCCATGG--CGTA
           ||  |    |||||||  ||        ||  ||||  |||| |||  |||  |||  |||
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                80              90             100             110             120             130             140
         GCGAATGAGTCGCAGGGTAGGAAGCCCACATGCGCAGTCAGTCCATGCGCCTG---ACC--TGTCGGTTGCGGCC
         |||||| ||| ||||||||| ||||||| ||||||||||| |||||| ||      ||   |||  ||   |||||
         GTGCAGGCCTGCAGGTTTAAAACGCGTATTCCTCACCGTTCAGCTTGATTACCTCATGTCCGAT-CG--C
         25490       25500       25510       25520       25530       25540       25550

                150             160             170             180             190             200
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         ||| |||    |||||||| ||||||||||  ||  ||  ||||  ||||||||||| |||||||||  |||||
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                210             220             230             240             250             260             270
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         ||||| ||||||||||||||||     ||   |||   ||     |||||||||||||| ||  ||||||||||
         TTTTCTTATCCA--AAGACAGCAGCTTCGC---TT----TAGCAGGC-GCTGTTTTG--CCTTCCTCCAGCCTA
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                280             290             300             310             320             330             340
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         ||| |||||||||||||||| ||| |||||||||||||||||||||| ||||||||||| ||||  |||
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                350             360             370             380             390             400             410
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         ||||||||||||| |||| |||||| |||||  ||||    |||||||||| |||||| ||||||| ||||
         ATTTCATACTTAGGATGCATTAGCTT--ATTGGGCAATTCCGCCGTCATTGGTTAAAAGCAAAAGACCGCTCG
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                420             430             440             450             460             470             480
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         || |||||||||||| |||||||  ||||||||| |||||  |       |||     |||||||||||||
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          550       560       570       580       590       600       610
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          CT---TCCGTTCAACCTTTAACCCGTTTACCTCAATC-TGATCAGAACCGGTGACCTTAACACCTAG--CT
          25970    25980    25990     26000    26010     26020     26030
          620       630       640       650       660                x
          CTAAAAGAAGTTTC--GTCA--TGGTATTTTCAGGCGTT-ATCAATTGCCGCATTATAGC
          ||    |||||| |||    |||||||||||   ||||||      |||| || || |||    x
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LOCUS       AE000308     11961 bp    DNA            BCT       01-DEC-2000
DEFINITION  Escherichia coli K12 MG1655 section 198 of 400 of the complete
            genome.
ACCESSION   AE000308 U00096
VERSION     AE000308.1  GI:1788508
KEYWORDS    .
SOURCE      Escherichia coli K12.
ORGANISM    Escherichia coli K12
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1  (bases 1 to 11961)
AUTHORS     Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau,B. and Shao,Y.
TITLE       The complete genome sequence of Escherichia coli K-12
JOURNAL     Science 277 (5331), 1453-1474 (1997)
MEDLINE     97426617
PUBMED      9278503
REFERENCE   2  (bases 1 to 11961)
AUTHORS     Blattner,F.R.
TITLE       Direct Submission
JOURNAL     Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   3  (bases 1 to 11961)
AUTHORS     Blattner,F.R.
TITLE       Direct Submission
JOURNAL     Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
            University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
            Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
            608-263-7459
REFERENCE   4  (bases 1 to 11961)
AUTHORS     Plunkett,G. III.
TITLE       Direct Submission
JOURNAL     Submitted (13-OCT-1998) Laboratory of Genetics, University of
            Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
COMMENT     This sequence was determined by the E. coli Genome Project at the
            University of Wisconsin-Madison (Frederick R. Blattner, director).
            Supported by NIH grants HG00301 and HG01428 (from the Human Genome
            Project and NCHGR). The entire sequence was independently
            determined from E. coli K12 strain MG1655. Predicted open reading
            frames were determined using GeneMark software, kindly supplied by
            Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
            30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that
            have been correlated with genetic loci are being annotated with CG
            Site Nos., unique ID nos. for the genes in the E. coli Genetic
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            Stock Center (CGSC) database at Yale University, kindly supplied by
            Mary Berlyn. A public version of the database is accessible
            (http://cgsc.biology.yale.edu). Annotation of the genome is an
            ongoing task whose goal is to make the genome sequence more useful
            by correlating it with other data.  Comments to the authors are
            appreciated. Updated information will be available at the E. coli
            Genome Project's World Wide Web site
            (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and
            its annotations are periodically updated; this is version M54. No
            sequence changes. Annotation updates: updated gene identifications
            and products; all new functional assignments courtesy of Monica
            Riley; added promoters, protein binding sites, and repeated
            sequences described in reference 1. The unique numeric identifiers
            beginning with a lowercase 'b' assigned to each gene (protein- or
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            labels. This should allow them to be searched for in Entrez as gene
            names.

FEATURES             Location/Qualifiers
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                /db_xref="GI:1788512"
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                /note="REP (repetitive extragenic palindromic) element;
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gene            complement(4567..5574)
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                /note="b2186"
CDS             complement(4567..5574)
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                N"
promoter        complement(5580..5608)
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promoter        5707..5734
                /note="factor Sigma70; predicted +1 start at 2282134"
gene            5756..5983
                /gene="yejL"
                /note="b2187"


CDS             5756..5983
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                /transl_table=11
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                /db_xref="GI:1788514"
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                /gene="yejM"
                /note="b2188"
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                /product="tRNA-Pro"
                /function="RNA; tRNA"
gene            7838..7914
                /gene="proL"
                /note="b2189"
gene            complement(8017..10527)
                /gene="yejO"
                /note="b2190"
CDS             complement(8017..10527)
                /gene="yejO"
                /function="putative transport; Not classified"
                /note="f836; This 836 aa ORF is 99 pct identical to
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                /transl_table=11
                /product="putative ATP-binding component of a transport
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                SLGKDTGTKVQANAVYDLGRSYQNGSITYSSKAISENMVINNGRANVWAGTMVNVSVR
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                AEAGTAVSYHMDLQNGTTLEPWLKAAVROEYADSNQVKVNDDGKFNNDVAGTSGVYQA
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promoter        10358..10386
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                  /gene="b2191"
CDS               10532..10654
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                  /function="orf; Unknown"
                  /note="o40; This 40 aa ORF is 38 pct identical (1 gap)
                  to31 residues of an approx. 384 aa protein ILEU_HUMAN SW:
                  P30740"
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                  /transl_table=11
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                  /db_xref="GI:1788517"
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promoter          complement(10539..10568)
                  /note="factor Sigma70; predicted +1 start at 2286925"
repeat_region     10546..11740
                  /note="IS5"
promoter          complement(10569..10597)
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gene              complement(10692..11708)
                  /gene="trs5_8"
                  /note="b2192"
CDS               complement(10692..11708)
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                  /function="IS, phage, Tn; Transposon-related functions"
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                  APSSTKNKEQQRDPEMHQIKKGNQWHFGMKAHIGVDAKSGLTHSLVTTAANEHDINQL
                  GNLLHGEEQFVSADAGYQGAPQREELAEVDVDWLIAERPGKVRTLKQHPRKNKTAINI
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ORIGIN
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AE000308  Length: 11961   September 24, 2001 09:20  Type: N  Check: 6916  ..

Initial Score    =    78    Optimized Score   =    291   Significance =   -0.78
Residue Identity =   49%    Matches           =    358   Mismatches   =    275
Gaps             =     95   Conservative Substitutions =               0
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                                        x          10
                            TCAGTTC--TCCTTAG---GGG
                            ||||||   | |||||   |||
AAATCCAAGAAAAAACCAACCTTACGGTTGGTTTTTTATATCTGCAATTAATTCGATAAACAGACCGTG
7920      7930      7940      7950      7960      7970      7980
      30        40        50        60        70        80
TAACATC-CCGCC-----ATTCCCCGTTTGCCAGCGGAGTCCAGCGTATAGCTGCCCATGGCGTAGCGAATGA
||||| |         |||||  || || ||||||||||||| ||||||||||| || |||||||| |||
ACACATTACAGCCTGTTTATTTTCTG-TTATCAGAACGTCCAGACCACCCGCC--TG-AGTATTCCA--C
7990      8000      8010      8020      8030      8040      8050
      90       100       110       120       130       140       150
GTCGCAGGGTAGGGAAGCCCACATGCCCAGTCAT-GC-GCCTGAC--CTG-TCGGTTGCGGCCTTCATAAAG
||| | ||  |  ||  |||   | ||  ||| ||| ||   | | || |  || ||| || |||| ||
GGCG-ATTCACCCCTGCGC-CAT-TGC---CATAGCTGACTGACAAATGACCGCTTAACGTCGGGGTAAAC
8060      8070      8080      8090      8100      8110
```

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                            160       170       180       190       200       210
GGTGATTTTAAGCCAG-CTGGTA---GGAA-TGGATTTACGCTCACGAATCGGCGGGTTGC--GCGGC---C
|||| |||||||||| | |||      ||| ||||||||||||||||||||  |||||||   ||||    |
GATGACCTTATACCAGCCTGATAAAACGCCACTGGTTCCAGCCACATCATTATTAAATTGCCATCGTCATTA
8120      8130      8140      8150      8160      8170      8180      8190
      220       230       240       250       260       270       280
ACAGCCACTCGGGTTCATTC-ACACGTTCAATACCAGC-CGGCAGGTGGGACCCGTCGTT-CAGCGTTACGC
|| |   ||||| ||||| | |||||||||| ||||| | |  |||||||||||| ||| | |||| |||||
ACTTTCACCTGGTTAGAATGGGCGTATTCCTGAC--GCACGAGCCCGTTCAGCCAGGGTTCCAGCGTCGTAC
8200      8210      8220      8230      8240      8250      8260
      290       300       310       320       330       340
CGTTGCGCAGCTTTGCCA-GCGA-CGCGT-CGTCCGGCTCGCCTTCAACCTGCACATA-GTAAATTTTTCCG
|||| || ||||||| || |||  ||||| |||||||||||||| |||||||||||||  ||||| |||| ||
CGTTTTGCAGGT---CCATGATAGCTTACCGCCGCCGTTCCGCCTTCAGCCGCGTA-ATATCGGGGTATTCC-
8270      8280      8290      8300      8310      8320
      350       360       370       380       390       400       410
GTACGTTTGCCCCGGCTG-AGTAAGCCTGGCCTGGAG--CACGCCCTCATTGGTAAGGACCAGCAGCCCCTCG
||  |||    ||| ||| |||||||||| || |||    |||||||| ||||| ||||| ||| |||| |
-CACATCCCGGCGCATGCCGTTTG-ATAACGTGTAGTCCTGACCATCTGTTGGTAAAG-CCGGTAAAGGCCCAG
8330      8340      8350      8360      8370      8380      8390
      420       430       440       450       460       470       480
CTGTTCGGATCCAGACGTCCCGCTGCGTAGACTCCCGTACGGGGATAAAGTCCT-TCAGCGTGCTGCGCCC
|| |   |   |||||  |||| || | ||||||| || || ||| ||| ||||  |||||||||| ||||
--ATAGGGTCTAACACTCCCCACAATCGTCAACCC---AACGG----AACCCGCTCAACATG-AGCACCC
8400      8410      8420      8430      8440      8450
      490       500       510       520       530       540       550
GGCTCGTCGGTAAACT--GCGGCAATACATCGTAG--GGTTATTGAAC--AGTATGACCCGCGTTGGC--
||  |        ||   |||   |  |  || |||   ||| | |     ||| |||||| ||| |||
-GCGCCGGTTACTATTGTAATCGCCAA-ACCGTGTTGCCCCCATTACTCATCTTGCCATGGATGGTGTTGGCAA
8460      8470      8480      8490      8500      8510      8520
      560       570       580       590       600       610       620
TGGGGT--TCTGGC-GTTCTTCTGTGGCTTGTC-GTGAGCTGAATCGCTCAACCCGGTGTTTTCTAAAG-
|| |     |||    |||||||||||| |||| ||||||| ||  || ||| ||| ||||||| |||
AACGGTCAACTTTGCCACCCACCCATCAACAATAGGCACCGTTCTGATGCTCCCAA-CCGGCATAAGCCCCCAGG
8530      8540      8550      8560      8570      8580      8590
      630       640       650       660
---AAGTTTTCGTCATGGTATTTTCAG--GCGTT----ATCAATTGCCCGCATTATAGC
   || ||||  || ||||||||||     ||||      |||||||| ||||||||||  x
GTATAGCTATCGGATATTACCTTTGCGCCCGGATCAAAAACCAATATCAGAATGAGAGTAACCAAAGATCAAG
8600      8610      8620      8630      8640      8650      8660      8670

CCGCCGAATTGTACTGCTTTCTTCACGGAGGAGAAACGG
8680      8690      8700
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6. US-09-252-691C-1394' (1-669)
   u00008     TOIG of: u00008     check: 8999   from: 1   to: 39149

   TOIG of: u00008   check: 8999   from: 1   to: 39149

   LOCUS       ECOHU49     39149 bp    DNA              BCT       10-FEB-1994
   DEFINITION  centisome 49 region of E.coli K12 BHB2600.
   ACCESSION   U00008
   VERSION     U00008.1   GI:453985
   KEYWORDS    .
   SOURCE      Escherichia coli K12 BHB2600.
   ORGANISM    Escherichia coli
               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
               Escherichia.
   REFERENCE   1  (bases 1 to 39149)
   AUTHORS     Richterich,P., Lakey,N., Gryan,G., Jaehn,L., Mintz,L., Robison,K.
               and Church,G.M.
   TITLE       Automated multiplex sequencing of the E.coli genome
   JOURNAL     Unpublished
   REFERENCE   2  (bases 1 to 39149)
   AUTHORS     Robison,K.
```

```
TITLE     Direct Submission
JOURNAL   Submitted (29-SEP-1993) Department of Genetics, Harvard Medical
          School, 200 Longwood Avenue, Boston MA 02115
REFERENCE 3 (bases 1 to 39149)
  AUTHORS Robison,K.
  TITLE   Direct Submission
  JOURNAL Submitted (10-FEB-1994) Department of Genetics, Harvard Medical
          School, 200 Longwood Avenue, Boston MA 02115
COMMENT   From E.coli K12 BHB2600.  All of the sequence in this contig was
          sequenced at least twice on one strand and once on the other
          strand, except in the 2 regions marked.  The annotation of this
          sequence should be considered preliminary and incomplete.  Please
          contact KRobison@nucleus.harvard.edu before citing this sequence
          in a published work.
FEATURES             Location/Qualifiers
          Region: Centisome 49.
     source          1..39149
                     /organism="Escherichia coli"
                     /db_xref="taxon:562"
     gene            <1..1230
                     /gene="yejA"
     CDS             <1..1230
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                     /note="probable transport operon; yejA-yejB/C-yejE-yejF.
                     Homologous to ABC-type transporters; closest similarity to
                     oliopeptide transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
                     /note="weak match to heme-binding protein from
                     H.influenzae"
                     /codon_start=1
                     /transl_table=11
                     /product="yejA"
                     /protein_id="AAA16375.1"
                     /db_xref="GI:453986"
                     /translation="DHKLSDPLATPLASGPYRVTSWKMGQNIVYSRVKDYWAANLPV
                     NRGRWNFDTIRYDYLDDNVAFEAFKAGAFDLRMENDAKNWATRYTDKKYIIKD
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                     TEYAARNYPDAAELVLLAPMKKDLPSEVFTQIYQPPVSKGDGYDRDNLLKADKLLNEA
                     GGVLKGQQRVNAATGQPLSFELLLPASSNSQWVLPFQHSLQRLGINMDIRKVDNSQIT
                     NRMRSRDYDMPRVWRAMPWPSSDLQISWSSEYINSTYNAPGVQSPVIDSLINQIIAA
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                     YDVNKAAKLPSASKQGE"
     CDS             1231..1620
                     /gene="yejB"
                     /note="probable transport operon; yejA-yejB/C-yejE-yejF.
                     Homologous to ABC-type transporters; closest similarity to
                     oliopeptide transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
                     /note="probable integral membrane component of transport
                     complex (oligopeptides?); C-terminus may be truncated to
                     form yejC"
                     /codon_start=1
                     /transl_table=11
                     /product="yejB"
                     /protein_id="AAA16376.1"
                     /db_xref="GI:405903"
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     gene            1487..2326
                     /gene="yejC -- probably a frameshift fragment of yejB"
     CDS             2326..3351
                     /gene="yejC"
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                     start and stop codons suggests translational coupling
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                     KPLLVRYDGSWYFPLLKNYSESDFGGPLASQADYQDPWLKQRLENNGWVLMAPIRFGA
                     TSINFATNKPFSPPSRQNWLGTDANGGDVLARILYGTRISVLGLMLTLCSSVMGVL
                     AGALQGYGKVDLWGQRFIEVWSGMPTLFLILLSSVVQPNFWLLAITVLFVGWMSL
                     VGVVRAEFLRTRNFDYIRAQALGVSDRSIILRHMLPNAMVATLTFPLPFILCSSITTL
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                     FDPNKAV"
     CDS             3353..4942
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                     Homologous to ABC-type transporters; closest similarity to
                     oliopeptide transporters.  Close proximity of inferred
                     start and stop codons suggests translational coupling
                     between all 4 genes."
                     /note="ABC-type ATP-dependent transport protein, perhaps
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                     ERQRVMIAMALLTRPELLIADEPTTALDVSVQAQIQLLRELQGELNMGMLFITHNLS
                     IVRKLAHRVAVMQNGRCVEQNYAATLFASPTHPYTQKLLNSEPSGDPVPLPEPASTLL
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                     /protein_id="AAA16380.1"
                     /db_xref="GI:405910"
                     /translation="MTSLQLSIVRHLPQNYRWSAGFAGSKVEPIPQNGPCGDNSLVAL
                     KLLSPGDNAWSVMYKLSQALSDIEVPCSVLECEGEPCLFVNRQDEFAATCRLKNFGV
                     AIAEPFSNYNPF"
     CDS             complement(5623..6756)
                     /note="bicyclomycin resistance gene"
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                     /transl_table=11
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                     /protein_id="AAA16406.1"
                     /db_xref="GI:424052"
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                     LMRDIYPKEEFSRMMSFVMLVTTIAPLMAPIVGGWLVWLSWHYIFWILALAAILASA
                     MIFFLIKETLPPERRQPHIRTTIGNFAALFRHKRVLSYMLASGFSFAGMFSFLSAGP
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                     MVISALLGLGFWSLVVAAFVGCVSMVSSNAMAVILDEFPHMAGTASSLAGTFRFGI
                     GAIVGALLSLATFNSAWPMIWSIAFCATSSILFCLYASRPKKR"
     CDS             complement(6841..7536)
                     /note="match to ORF from B.subtilis; weaker match to ORF
                     from Buchnera aphidicola and orf near centisome 89"
                     /codon_start=1
                     /transl_table=11
                     /product="yejD"
                     /protein_id="AAA16377.1"
                     /db_xref="GI:405907"
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CDS        7156..7659
           /note="probably not expressed; yejD on opposite strand has
           better dicodon usage"
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           /protein_id="AAA16407.1"
           /db_xref="GI:405943"
           /translation="MAARRSNAVRPLTIISHQHTGGINIOPPRRMQFPRYRFIKKIE
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           IAADFTPGNSTANAELLCDKFIKSHVCDFACKNGGRALTRKSELLSAQYSLITSLKG
           KRSMAYY"

CDS        7685..8896
           /note="some similarity to a phage protein and
           restriction-modification systems"
           /codon_start=1
           /transl_table=11
           /product="yejH"
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           /db_xref="GI:405911"
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           IYQFHYMVRGDEKALFRDCIYELPLRYMIKHGYLTPPERLDMPVVQVDFSRLQAQS
           NGLFSEADLNRELKKQQRITPHIISQIMEFAATRKGVMIFAATVEHAKEIVGLLPAED
           AALITGDTPGAERDVLIENFKAQRFRYLVNVAVLTGFDAPHVDLIAILRPTESVSLY
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gene       8812..9162
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gene       9117..9446
           /gene="yejJ -- may be frameshift fragment"

CDS        9571..9861
           /note="ribosomal protein L25"
           /codon_start=1
           /transl_table=11
           /product="rplY"
           /protein_id="AAA16413.1"
           /db_xref="GI:405949"
           /translation="MFTINAEVRKEQGKGASRLRAANKFPAIIYGGKEAPLAIELDH
           DKVMNMQAKAEFYSEVLTIVVDGKEIKVKAQDVQRHPYKPKCSTSTSFALNC"

repeat_region  9949..9985
           /rpt_family="REP/PU"

CDS        complement(9993..11000)
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           /transl_table=11
           /product="yejK"
           /protein_id="AAA16382.1"
           /db_xref="GI:405914"
           /translation="MSLDINQIALHQLIKRDEQNLELVLRDSLLEPTETVVEMVAELH
           RVYSAKNKAVGLFSEESELAQTLRLQRQGEEDFLAFSRAATGRLRDELAKYPFADGGF
           VLFCHYRYLAVEYLLVAVLSNLSSMRVNENLDINPTHYLDINHADIVARIDLTEWETN
           PESTRYLTFLKGRVGRKVADFFMDFLGASEGLNAKAQNRGLLQAVDDFTAEAQLDKAE
           RQNVRQQVYSYCNEQLQAGEEIELKSLSKELAGVSEVSFTEFAAEKGYELEESFPADR
           STLRQLFKFAGSGGGLTINFDAMLLGERIFWDPATDTLTIKGTPPNLRDQLQRRTSGG
           N"

CDS        11182..11409
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           /transl_table=11
           /product="yejL"
           /protein_id="AAA16383.1"
           /db_xref="GI:405915"
           /translation="MPQISRYSDEQVEQLLAELLNVLEKHKAPTDLSLMVLGNMVTNL
           INTSIAPAQRQAIANSFARALQSSINEDKAH"

CDS        11429..13189
           /codon_start=1
           /transl_table=11
           /product="yejM"
           /protein_id="AAA16384.1"
           /db_xref="GI:453987"
           /translation="MVTHRQRYREKVSQMVSWGHWFALFNILLSLVIGSRYLFIADWP
           TTLAGRIYSYSIIGHFSFLVFATYLLILFPLTFIVGSQRLMRFLLSVILATAGMTLLL
           IDSEVFTRFHLHLNPIVWQLVINPDENEMARDWQLMFISVPVILLELVFATWSWQKL"
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RSLTRRRFARPLAAFLFIAFIASHVVYIWADANFYRPITMQRANLPLSYPMTARRFL
EKHGLLDAQEYQRRLIEQGNPDAVSVQYPLSELRYRDMGTGQNVLLITVDGLNYSRFE
KQMPALAGFAEONISFTRHMSSGNTTDNGIFGLFYGISPSYMDGILSTRTPAALITAL
NQQGYQLGLFSSDGFTSPLYRQALLSDFSMPSVRTQSDEQTATQWINWLGRYAQEDNR
WFSWVSFNGTNIDDSNQQAFARKYSRAAGNVDDQINRVLNALRDSGKLDNTVVIITAG
RGIPLSEEEETFDWSHGHLQVPLVIHWPGTPAQRINALTDHTDLMTTLMQRLHVSTP
ASEYSQGQDLFNPQRRHYWVTAADNDTLAITTPKKTLVLNNNGKYRTYNLRGERVKDE
KFQLSLLQVLTDEKRFIAN"

tRNA       13264..13346
           /gene="proL"
           /note="codon recognized: CCC"
           /product="tRNA-Pro"

gene       13264..13346
           /gene="proL"

CDS        complement(13443..16010)
           /partial
           /note="strong match to pertactin from Bordetella.  No
           start codonmay be missing some of N-terminus"
           /codon_start=1
           /transl_table=11
           /product="yejO"
           /protein_id="AAA16385.1"
           /db_xref="GI:405918"
           /translation="VSREEFPRLFAPSLYSPIALASTVEYGETVDGVVLEKDIQLVYG
           TANNTKINPGGEQHIKEFGVSNNTEINGGYQYIEMNGAAEYSVLNDGYQIVQMGGAAN
           QTTLNNGVLQVYGAANDTTIKGGRLIVEKDGGAVFVAIEKGGLLEVKEGGFAFAVDQK
           AGGAIKTTRAMEVFGTNRLGQFDIKNGIANNMLLENGGSLRVEENDEFAYNTTVDSGG
           LLEVMDGGTVTGVDKKAGGKLIVSTNALEVSGPNSKGQFSIKDGVSKNYELDDGSGLI
           VMEDTQAIDTILDKHATMQSLGKDTGTKVQANAVYDLGRSYQNGSITYSSKAISENMV
           INNGRANVWAGTMVNVSVRGNDGILEVMVGVRGNDGILEVMGYINYAPAMLVGKVVVSEGASFRTHGAVD
           TSKADVSLENSVWTIIADITTNQNTLLNLANLAMSDANVIMMDEPVTRSSVTASAEN
           FITLTTNTLSGNGNFYMRTDMANHQSDQLNVTGQATGDFKIFVDTGASPAAGDSLTL
           VTTGGDAAFTLGNAGGVVDIGTYEYTLLDNGNHSWSLAENRAQITPSTTDVLNMAAA
           QPLVFDAELDTVRERLGSVKGVSYDTAMWSSAINTRNNVTTDAGAGFEQTLTGLTGI
           DSRFSREESSTIRGLIFGYSHSDIGFDRGGKGNIDSYTLGAYAGWEHQNGAYDVDGVK
           VDRFANTHGKMSNGATAFGDYNSNGGAAHVESGFRWVDGLSVRPYLAFTGFTTDGQ
           DYTLSNGMRADVGNTRILRAEAGTAVSYIHMDLQNGTTLEPWLKAAVRQEYADSNQKV
           NDDGKFNNDVAGTSGVVQAGIRSSFTPTLSGHLSVSYGNGAGVESPWNTQAGVVWTF"

repeat_unit  15970..17170
           /rpt_family="IS5"

CDS        17523..18200
           /note="regulatory protein narP"
           /codon_start=1
           /transl_table=11
           /product="narP"
           /protein_id="AAA16411.1"
           /db_xref="GI:405947"
           /translation="MILIKPQETTMPEATPFQYMIVDHPLMRRGVRQLLELDPGSEV
           VAEAGDGASAIDLANRLDIDVILLDLNMKGMSGLDTLNALRRDGVTAQIIILTVSDAS
           SDVFALIDAGADGYLLKDSDPEVLLEAIRAGAKGSKVFSERVNQYLREREMFGAEEDP
           FSVLTERELDVLHELAQGLSNKQIASVLNISEQTVKVHIRNLLRKLNVRSRVAATILF
           LQQRGAQ"

repeat_region  18231..18385
           /rpt_family="REP/PU"

CDS        complement(18411..19463)
           /note="probably part of aeg-46.5 operon; homolog of
           Rhodobacter ccl2"
           /codon_start=1
           /transl_table=11
           /product="yejP"
           /protein_id="AAA16386.1"
           /db_xref="GI:405919"
           /translation="MRFLLGVLMLMISGSALATIDVLQFKDEAQEQQFRQLTEELRCP
           KCQNNSIADSNSMIATDLRQKVYELMQEGKSKKEIVDIMVARYGNFVTYDPPLPLTV
           LLWVLPVVAIGICGGWVIYARSRRVRVVPEAFPEQSVPEGKRAGYVVYLPGIVVALIV
           AGVSYYQTIGNYQQVKIWQQATAQAPALLDRALDPKADPLNEEEMSRALGMRTQLQKN
           PGDIEGWIMLGRVGMALGNASIATDAYATAYRLDPKNSDAALGYAEALTRSSDPNDNR
           LGGELLRQLVRTDHSNRIRVLSMYAFNAFEQQRFGEAVAAWEMMKLLPANDTRRAVIE
           RSIAQAMQHLSPQESK"

CDS        complement(19960..20017)
           /note="probable thioredoxin; may be part of aeg-46.5
           operon"
           /codon_start=1
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CDS
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                    /transl_table=11
                    /product="yejQ"
                    /protein_id="AAA16387.1"
                    /db_xref="GI:405920"
                    /translation="MKRKVLLIPLIFLAIAAALLWQLARNAEGDDPTNLESALIGKP
                    VPKFRLESLDNPGQPYQADVLTQGKPVLLNVWATWCPTCRAEHQYLNQLSAQGIRVVG
                    MNYKDDRQKAISWLKELGNPYALSLFDGDGMLGLDLGVYGAPETFLIDGNGIIRYRHA
                    GDLNPRVWEEIKPLWEKYSKEAAQ"
     complement(20014..21957)
                    /note="may be part of aeg-46.5 operon; strong match to
                    cell from Rhodobacter and corresponding plastid proteins"
                    /codon_start=1
                    /transl_table=11
                    /product="yejR"
                    /protein_id="AAA16388.1"
                    /db_xref="GI:405921"
                    /translation="MMPEIGNGLLCLALGIALLLSVYPLMGVARGDARMMASSRLFAW
                    LLFMSVAGAFLVLVLNAFVVNDFTVTYVASNSNTQLPVWYRVAATWGAHEGSLLLWVLL
                    MSGWTFAVAIFSQRIPLDIVARVLAIMGMVSVGFLLFILFTSNPFSRTLPNFPIEGRD
                    LNPLLQDPGLIFHPPLLYMGYVGFSVAFAFAIASLLSGRIDSTYARFTRPWTLAAWIF
                    LTLGIVLGSAWAYELGWGWGWNFDPVENASFMPWLVGTALMHSLAVTEQRASFKAWT
                    LLAISAFSLCLLGTFLVRSGVLVSVHAFASDPARGMFILAFMVLVIGGSLLLFAARG
                    HKVRSRVNNALWSRESLLLANNVLLVAAMLVVLLGTLEPLIVHKQLGLGSLSIGEPFFN
                    TMFTWLMVPFALLLGVFPLVRWGRDRPRKIRNLLIIAFISTLVLSLLLPWLFESKVVA
                    MTVLGLAMACWIAVLAIAEAALRISRGKTKTFSYWGMVAAHLGLAVTIVGIAFSQNYS
                    VERDVRMKSGDSVDIHEYRFTFRDVKEVTGPNWRGGVATIGVTRDGKPETVLIAEKRY
                    YNTAGSMMTEAAIDGGITRDLYAALGEEELENGAWAVRLYYKPFVRWIWAGGLMMALGG
                    LLCLFDPRYRKRVSPQKTAPEAV"
     complement(21954..22433)
                    /note="may be part of aeg-46.5 operon"
                    /codon_start=1
                    /transl_table=11
                    /product="yejS"
                    /protein_id="AAA16389.1"
                    /db_xref="GI:405922"
                    /translation="MNIRRKNRLWIACAVLAGLALTIGLVLYALRSNIDLFYTPGEIL
                    YGKRETQQMPEVGQRLRVGGMVMPGSVQRDPNSLKVTFTIYDAEGSVDVSYEGILPDL
                    FREGQSVVQGELEKGKNHILAKEVLAKHDENYTPPEVEKAMEANHRRPASVYKDPAS"
     complement(22430..22639)
                    /codon_start=1
                    /transl_table=11
                    /product="yojM"
                    /protein_id="AAA16390.1"
                    /db_xref="GI:453988"
                    /translation="MTPAFASWNEFFAMGGYAFFVWLAVVMTVIPLVVLVVHSVMQHR
                    AILRGVAQQRAREARLRAAQQOEAA"
gene  complement(22636..22977)
                    /gene="yejT -- may be frameshift fragment"
CDS   complement(22881..23372)
                    /note="homolog of helC from Rhodobacter; probably part of
                    aeg-46.5 operon"
                    /codon_start=1
                    /transl_table=11
                    /product="yejU"
                    /protein_id="AAA16391.1"
                    /db_xref="GI:405924"
                    /translation="MWKTLHQLAIPPRLYQICGWFIPWLAIASVVLTVGWIWGFGFA
                    PADYQQGNSYRIIYLHVPAAIWSMGIYASMAVAAFIGLVWQMKMANLAVAAMAPIGAV
                    FTFIALVTGSAWGKPMWGTWWVWDARLJTSELVLFLYVGVIALMWHAFDDRRLAAVRQV
                    SWC"
CDS   complement(23414..24076)
                    /note="may be part of aeg-46.5 operon; homolog of
                    Rhodobacter helB and corresponding plastid proteins"
                    /codon_start=1
                    /transl_table=11
                    /product="yejV"
                    /protein_id="AAA16392.1"
                    /db_xref="GI:405925"
                    /translation="MMFWRIFRLELRVAFRHSAEIANPLWFFLIVITLFPLSIGPEPQ
                    LLARIAPGIIWVAALLSSLLALERLFRDDLQGSLEOLMLLPLPAVVLAKVMAHWM
                    VTGLPLLLSPLVAMLLGMDVYGWQVMALTLLGTPTLGFLGAPGVALTVGLKRGGVL
                    LSILVLPLTIPLLIFATAMDAASMHLPVDGYLAILGALLAGTATLSPATAAALRIS
                    IQ"
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CDS
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     complement(24073..24690)
                    /note="ABC-type ATP-dependent transporter; may be part of
                    aeg-46.5 operon"
                    /codon_start=1
                    /transl_table=11
                    /product="yejW"
                    /protein_id="AAA16393.1"
                    /db_xref="GI:405926"
                    /translation="MLEARELLCERDERTLFSGLSFTLNAGEWVQITGSNGAGKTLL
                    RLLTGLSRPDAGEVLWQGQPLHQVRDSYHQNLLWIGHQPGIKTRLTALENLHFYHRDG
                    DTAQCLEALAQAGLAGFEDIPVNQLSAGQQRRVALARLWLTRATLWILDEPTAIDVN
                    GVDRLTQRMAQHTEQGGIVILTTHQPLNVAESKIRRISLTQTRAA"
     complement(24709..25311)
                    /note="may be part of aeg-46.5 operon; strong similarity
                    to nirT from P.stutzeri"
                    /codon_start=1
                    /transl_table=11
                    /product="yejX"
                    /protein_id="AAA16394.1"
                    /db_xref="GI:405927"
                    /translation="MGNSDRKPGLIKRLWKKWRTPSRLAGTLLLIGFVGGIVFWGGF
                    NTGMEKANTEEFCISCHEMRNTVYQEXMDSVHYNNRSGVRATCPDCHVPHEFVPKMIR
                    KLKASKELYGKIFGVIDTPQKFEAHRLTMAQNEWRMKDNNSQECRNCHNFEYMDTTA
                    QKSVAAKMHDQAVKDGQTCIDCHKGIAHKLPDMREVEPGF"
     complement(25281..25790)
                    /note="may be part of aeg-46.5 operon; match to
                    periplasmic nitrate reductase B subunit (napB) from
                    Alcaligenes eutrophus; weak match to Human guanylate
                    cyclase"
                    /codon_start=1
                    /transl_table=11
                    /product="yejY"
                    /protein_id="AAA16395.1"
                    /db_xref="GI:405928"
                    /translation="MEFGSEIMKSHDLKKALCQWTAMLALVVSGAVWAANGVDFSQSP
                    EVSGTOEGAIRMPKEQDRMPLNYVNQPPMIPHSVEGYQVTNTNRCLQCHGVESYRTT
                    GAPRISPTHFMDSDGKVGAEVAPRRYFCLQCQYRRPIPRQSWGIPLPHQKTVGNKRLL
                    WEILTVSLV"
     complement(25766..26629)
                    /note="may be part of aeg-46.5 operon; weak match to
                    ferredoxins"
                    /codon_start=1
                    /transl_table=11
                    /product="yejZ"
                    /protein_id="AAA16396.1"
                    /db_xref="GI:405929"
                    /translation="MANRKRDAGREALEKKGWRSHRWLVLRRLCQFFVLGMFLSGPW
                    FGVWIIHGNYSSSLLFDTVPLTDPLMTLQSLASGHLPATVALTGAVIITVLYALAGKR
                    LFCSWVCPLNPITDLANWLRRRFDLNQSATIPRHIRYVLLVVILVGSALTGTLIWEWI
                    NPVSLMGRSLVMGFGSGALLILALFLFDLLVEHGWCGHICPVGALYGVLGSKGVITV
                    AATDRQKCNRCMDCFHVCPEPHVLRAPVLDEQSPVVTSRDCMTCGRCVDVCSEDVFT
                    ITTRWSSGAKS"
     complement(26616..27008)
                    /note="possible ferredoxin; GTG start codon; may be part
                    of aeg-46.5 operon"
                    /codon_start=1
                    /transl_table=11
                    /product="yojA"
                    /protein_id="AAA16397.1"
                    /db_xref="GI:405930"
                    /translation="MRTFRAPKCAQAVRWIVRLNRSTTRGWGWRWTWTRKTVSTFRGL
                    RCDVCYRECPKIDEAITLELERNTRTGKHAARFLPTVHSDACTGCGKCEKVCVLEQPAI
                    KVLPLSLAKGELGHHYRFGWLEGNNGKS"
     complement(26839..27312)
                    /note="may be part of aeg-46.5 operon; weak match to
                    several proteins with redox functions"
                    /codon_start=1
                    /transl_table=11
                    /product="yojB"
                    /protein_id="AAA16398.1"
                    /db_xref="GI:405931"
                    /translation="MSRSAKPQNGRRRFLRDVVRTAGGLAAVGVALGLQQOTARASGV
                    RLRPPGAINENAFASACVRCGQCVQACPYDTLKLATLASGLSAGTPYFVARDIPCEMC
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     CDS             EDIPCAKVCPSGALDREIEISIDDARMGLAVLVDQENCLNFQGPALRCLLSRMPEN"
                     complement(27319..29748)
                     /note="may be part of aeg-46.5 operon; strong match to the
                     periplasmic nitrate reductase large subunit (napA) from
                     Alcaligenes eutrophus; GTG start codon"
                     /codon_start=1
                     /transl_table=11
                     /product="yojC"
                     /protein_id="AAA16399.1"
                     /db_xref="GI:453989"
                     /translation="MPVSACRAVARAVVGQQEAIKWDKAPCRFCGTGCGVLVGTQQGR
                     VVACQGDPAPVNRGLNCIKGYFLPKIMYGKDRLRQPLLRMKNGKYDKEGEFTPITWD
                     QAFDVMEEKFKTALKEKGPESIGMFGSGQWTIWEGYAASKLFKAGFRSNNIDPNARHC
                     MASAVVGFMRRIFGMDEPMGCYDDIEQADAFVLWGANMAEMHPILWSRITNRRLSNQNV
                     TVAVLSTYQHRSFELADNGIIFTPQSDLVILTNYIANYIIONNAINQDFFSKHVNLRKG
                     ATDIGYGLRPTHPLEKAAKNPGSDASEPMSFEDYKAFVAEYTLEKTAEMTGVPKDQLE
                     QLAQLYADPNKKVISSWTMGFNQHTRGVWANNLVYNLHLLTGKISQPGCGPFSLTGQP
                     SACGTAREVCTFAHRLPADMVVTNEKHRDICEKKWNIPSGTIPAKIGLHAVAQDRALK
                     DGKLNVYWTMCTNNMQAGPNINEERMPGWRDPRNFIIVSDPYPTVSALAADLILPTAM
                     WVEKEGAYGNAERRFQFWRQQVQAPGEAKSDLWQLVQFSRRFKTEVWPEDLLAKKPE
                     LRGKTLYEVLYATPEVSKFPVSELAEDQLNDESRELGFYLQKGLFEEYAWFGRGHGHD
                     LAPFDDYHKARGLRMPVVNGKETQWRYSEGNDPYVKAGEGYKFYGKPDGKAVIFALPF
                     EPAAEAPDEEYDLWLSTGRVLEHWHTGSMTRRVPELHRAFPEAVLFIHPLDAKARDLR
                     RGDKYKVSRRGEVISIVETRGRNRPPQGLVYMPFFDAAQLVNKLTLDATDPLSKETD
                     FKKCAVKLEKV"

     misc_feature    29705..29859
                     /note="CAUTION! Low coverage in this region of the
                     sequence"
                     /note="Region: Area of low coverage 2"

     CDS             complement(29801..30064)
                     /note="may be part of aeg-46.5 operon"
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                     /db_xref="GI:405935"
                     /translation="MHTNWQVCSLVVQAKSERISDISTQLNAFPGCEVAVSDAPSGQL
                     IVVVEAEDSETLIQMIESVRNVEGVLAVSLVYHQQEQGETP"

     CDS             complement(30054..30548)
                     /note="probable ferredoxin or Fe-S protein; probably part
                     of aeg-46.5 operon"
                     /codon_start=1
                     /transl_table=11
                     /product="yojG"
                     /protein_id="AAA16401.1"
                     /db_xref="GI:453990"
                     /translation="MKIDASRRGILTGRWRKASNGIRPPWSGDESHFLTHCTRCDACI
                     NACENNILQRGAGGYPSVNFKNNECSFCYACAQACPESLFSPRHTRAWDLQFTIGDAC
                     LAYQSVECRRCQDSCEPMAIIFRPTLSGIYQPQLNSQLCNCGCACAASCPVSAITAEY
                     LHAH"

     CDS             30935..31444
                     /note="DNA repair protein"
                     /codon_start=1
                     /transl_table=11
                     /product="ecotin (protease inhibitor)"
                     /protein_id="AAA16410.1"
                     /db_xref="GI:453992"
                     /translation="MKKESKKMKTILPAVLFAAFATTSAWAAESVQPLEKIAPYPQAE
                     KGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYVFD
                     KVSSPVSTMMACPDGKKEKKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRWKAE
                     EKIDNAVVR"

     repeat_region   31533..31654
                     /rpt_family="REP/PU"
     repeat_region   31689..31711
                     /rpt_family="REP/PU"
     repeat_region   31814..31845
                     /rpt_family="REP/PU"
     repeat_region   31875..31981
                     /rpt_family="REP/PU"
     repeat_region   31973..32018
                     /rpt_family="REP/PU"
     repeat_region   32030..32096
                     /rpt_family="REP/PU"

     CDS             complement(32159..33631)
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                     /transl_table=11
                     /product="yojH"
                     /protein_id="AAA16402.1"
                     /db_xref="GI:424051"
                     /translation="MTMVERLEGVAQESSNGWNNAGTGHSALMELNYTPQNADGSISI
                     EKAVAINEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDNVNFLRARYAAL
                     QQSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQOKVAATRTEIGTDVNYGEITRQLIAS
                     LQKKSNFSLQLSSEVRALKRNDNTWTVTVADLKNGTAQNIRAKFVFIGAGAALKLL
                     QESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVVGKASVGAPPMSVPHIDTRVLD
                     GKRVVLFGPAFTSTKFLKNGSLMDLMSSTTSNVMPMHVGLDNFDLVKYLVSQVML
                     SEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLRLGTEVVSDQOGTIA
                     ALLGASPGASTAPIMLNLLEKVFGDRVSSPQWOATLKAIVPSYGRKLNGDVAATERE
                     LQYTSEVLGLNYDKPQOADSTPKPQLKPQPVQKEVADIAL"

     CDS             complement(34023..35666)
                     /note="ABC-type ATP-dependent transport protein. Match to
                     syrD from Pseudomonas syringae over most of length and
                     outside ABC-family signatures."
                     /codon_start=1
                     /transl_table=11
                     /product="yojI"
                     /protein_id="AAA16403.1"
                     /db_xref="GI:453991"
                     /translation="MELLVLVWRQYRWPFISVMALSLASAALGIGLIAFINQRLIETA
                     DTSLLVLPEFLGLLLLMAVTLGSQLALTTLGHHFVYRLRSEFIKRILDTHVERIEQL
                     GSASLLAGLTSDVRNITIAFVRLPELVQGIILTIGSAAYLWMLSGAKLMLLVTAIWMAIT
                     IWGGFVLVARVYKHMATLRETEDKLYTDFQTVLEGRKELTLNRERAEYVFNNLYIPDA
                     QEYRHIIRADTFHLSAVNWSNIMMLGAIGLVFWMANSLGWADTNVAATYSLTLLFLR
                     TPLLSAVGALPTLTAQVAFNKLNKFALAPFKAEFPRPQAFPNWQTLERNVTFAYQD
                     NAFSVGPINLTIKRGELLFLIGGNGSGKSTLAMLLTGLYQPQSGEILLDGKPVSGEQP
                     EDYRKLFSAVFTDVWLFDQLLGPEGKPANPQLVEKWLAQLKMAHKLELSNGRIVNLKL
                     SKGQKKRVALLALAEERDIILLDEWAADQDPHFRREFYQVLLPLMQEMGKTIFAISH
                     DDHYFIHADRLLEMRNGQLSELTGEERDAASRDAVARTA"

     CDS             complement(35742..36392)
                     /codon_start=1
                     /transl_table=11
                     /product="alkB"
                     /protein_id="AAA16409.1"
                     /db_xref="GI:405945"
                     /translation="MLDLFADAEPWQEPLAAGAVILRRAFNAEQLIRDINDVASQS
                     PFRQMVTPGGYTMSVAMTNCGHLGWTTHRQYLYSPIDPQTNKPWPAMPQSFINLCQR
                     AATAAGYPDFQPDACLINRYAPGAKLSLHQDKDEPDLRAPIVSVSLGLPAIFQFGGLK
                     RNDPLKRLLEHGDVVWGGESRLFYHGIQPLKAGFHPLTIDCRYNLTFRQAGKKE"

     CDS             complement(36392..37456)
                     /note="DNA repair protein"
                     /codon_start=1
                     /transl_table=11
                     /product="ada"
                     /protein_id="AAA16408.1"
                     /db_xref="GI:405944"
                     /translation="MKKATCLTDDQRWQSVLARDPNADGEFVFAVRTTGIFCRPSCRA
                     RHALRENVSFYANASEALAAGFRPCKRCQPEKANAQOHRLDKITHACRLLEQETPVTL
                     EALADQVAMSPFHLHRLFKATTGMTPKAWOQAWRARRLRESLAKGESVTTSLNAGFP
                     DSSSYYRKADETLGMTAKQFRHGGENLAVRYALADCELGRCLVAESERGICAILLGDD
                     DATLISELQQMFPAADNAPADLMFQQHVREVIASLNQRDTPLTLPLDIRGTAFQOQVM
                     QALRTIPCGETVSYQOLANAIGKPKAVRAVASACAANKLAIIIPCHRVVRGDCTLSGY
                     RWGVSRKAQLLRREAENEER"

     misc_feature    36978..37132
                     /note="CAUTION! Low coverage in this region of the
                     sequence"
                     /note="Region: Area of low coverage 1"

     CDS             complement(37530..38112)
                     /note="weak match to rnfF from Rhodobacter capsulatus"
                     /codon_start=1
                     /transl_table=11
                     /product="yojK"
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                     /db_xref="GI:405940"
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BASE COUNT   9381 a   10833 c   9785 g   9150 t
ORIGIN

U00008   Length: 39149   September 24, 2001 09:20   Type: N   Check: 8999   ..

Initial Score   =   78   Optimized Score   =   291   Significance = -0.78
Residue Identity   =   49%   Matches   =   358   Mismatches   =   275
Gaps   =   Conservative Substitutions =   95   =   0

                                      x   10
                        TCAGTTC--TCCTTAG--GGG
                        | | | | | | || |
AAATCCCAGAGAAAAAACCAACCTTACGGTTGTGTTTTTATATCTGCAATTAATTCGATAAAACAGACCGTG
     13350   13360   13370   13380   13390 x   13400   13410
20   30   40   50   60   70   80
TAACATC-CCGCC-----ATTCCCGTTGCCAGCGAGTCCAGCGTATAGCTGCCCATGGGCGTAGCGAATGA
     |||| | ||| ||| ||| ||| |||| ||||| || | ||| ||| | |||
ACACATCACAGCCGTTGTTATTTTCTG-TTATCAGAACGTCCAGAACAACCACCCGCC--TG-AGTATTCCA--C
     13420   13430   13440   13450   13460   13470
90   100   110   120   130   140   150
GTCGCAGGGTAGGGAAGCCACATGCCAGTCAT-GC-GCCTGAC--CTG-TCGGTTGCGGCCTTCATAAAG
     | | || || | || ||| | ||| || | | | | ||| | | | | | | ||||
GGCG-ATTCTACCCCTGCGC-CAT-TGC---CATAGCTGACTGACAAAATGACCGCTTAACGTCGGGGTAAAC
     13480   13490   13500   13510   13520   13530   13540
160   170   180   190   200   210
GGTGATTTTAAGCCAG-CTGGTA---GGAA-TGGATTTACGCTCACGAATCGGCGGGTTGC--GCGGC---C
     | ||| ||| ||| ||| || | || |||| | |||| |||| ||||| | ||| ||
GATGACCTTATACCAGCCTGATAAACGCCACTGGTTCCAGCCACATCATTATTAAATTGCCATCGTCATTA
     13550   13560   13570   13580   13590   13600   13610
220   230   240   250   260   270   280
ACAGCCACTCGGGTTCATTC-ACACGTTCAATACACAGC-CGGCAGGGTGGGACCGGTCGTT-CAGCGTACGC
     || | || || | | | || ||||| || | ||| | ||||| | || | ||||||||
ACTTTCACCTGGTTAGAATCGGCGTATTCCTGAC--GCACCGCCGCGCTTCAGCCAGGGTTCCAGCGTCGTAC
     13620   13630   13640   13650   13660   13670   13680
290   300   310   320   330   340
CGGTTGCGCAGCTTTGCCA-GCGA-CGCGT-CGTCCCGGCTCGCCTTCAACCTTCGCACATA-GTAAATTTTTCCG
     ||||| ||| |||| | |||| | ||| | || || | || || ||| |||| | ||||||
CGTTTTGCGAGGT---CCATGTGATAGCGTTACCGCCGTTCCCGCTTCAGCGGGTA-ATATCCGGGGTATTTCC-
     13690   13700   13710   13720   13730   13740   13750
350   360   370   380   390   400   410
GTACGTTTGCCCGGCTG-AGTAAGCCTGGCCTGGAG--CACGCCGTCATTGGTAAGGACCAGCAGCCCCTCG
     | ||| || || ||| || | |||| | ||| ||| | | | | | |||| | | || ||||||
-CACATCCGCGCGCATGCCGTTGG---CCGATTGCTGTAATAACGTGTAGTCCTTGACCATCTGTGGTAAAG-CCGGTAAAGGCCAG
     13760   13770   13780   13790   13800   13810   13820
420   430   440   450   460   470   480
CTGTCGCGGATCCAGACCTCCCCGCTGCCTGAGATCCCCGTACGGGGGATAAAGTCCT-TCAGCGTGCTGCGCCCC
     | | ||| || ||| |||| | ||| | | ||| || || || || | ||| || || |||| ||

--ATAGGGTCTAACACTCCCACAATCGTCAACCC----AACGG----AACCCGCTCTCAACATG-AGCACCC
     13830   13840   13850   13860   13870   13880
490   500   510   520   530   540   550
GGCCTGCGTCGGTAAACT--GCGGCAATACATCGTAG--GGTTTATTGAAC--AGTATGACCCGCGTTGGC--
     ||| ||| ||||| ||| || | || ||| | | ||| ||| || || | || | ||| |||||||
-GCGCCGGTTACTATTGTAATCGCCAA-ACGCTGTTGCCCCATTACTACTTCTTGCCATGGATGGTGGTTGGCAA
     13890   13900   13910   13920   13930   13940   13950
560   570   580   590   600   610   620
TGGGT-TCTGGC-GTTCTTCGGTGGCTTGTC-GTGAGCTGAATCGCTCAACCCGGTGTTTTCTAAAAG-
     | | | ||| | ||| ||| | | | ||||| || | | | | |||||| ||| | |||||| |||
AACGGTCAACTTTCACCACCCATCAACATAGGCACCGTTCTGATGCTCCCAA-CCGGGCATAGCCCCCAGG
     13960   13970   13980   13990   14000   14010   14020
630   640   650   660
---AAGTTTCGTCATGGTATTTTCAG--GCGTT----ATCAATTGCCGCATTATAGC   x
     | | ||||| | | | | || || | | ||| | || ||| | || ||| |||||||
GTATAGCTATCGATATTACCTTTCGCCGCCGGATCAAAAACCAATATCAGAATCAGAGTAACCAAAGATCAAG
     14030   14040   14050   14060   14070   14080 x   14090

CCGCGAATTGTACTGCTTTCTTCACGGGAGAAACGG
     14100   14110   14120   14130

7. US-09-252-691c-1394' (1-669)
     109228   TOIG of: 109228   check: 8816   from: 1   to: 28206

TOIG of: 109228   check: 8816   from: 1   to: 28206

LOCUS   BACDIA   28206 bp   DNA   BCT   26-MAY-1995
DEFINITION   Bacillus subtilis spoVA to serA region.
ACCESSION   L09228
VERSION   L09228.1   GI:410114
KEYWORDS   3-dehydroquinate dehydratase; aroC gene; diaminopimelate
             decarboxylase; lysA gene; penicillin-binding protein;
             peptidyl-prolyl isomerase; phosphoglycerate dehydrogenase; ppiB
             gene; response regulator; response regulator kinase; riba gene;
             ribB gene; ribD gene; ribG gene; ribH gene; ribT gene; riboflavin
             biosynthesis operon; serA gene; signal peptidase; sips gene; spoA
             gene; spoVAF gene.
SOURCE   Bacillus subtilis (strain 168, sub_species Marburg) DNA.
ORGANISM   Bacillus subtilis
             Bacteria; Firmicutes; Bacillus/Clostridium group;
             Bacillus/Staphylococcus group; Bacillus.
REFERENCE   1 (bases 1 to 28206)
AUTHORS   Yamamoto,J., Shimizu,M. and Yamane,K.
TITLE   Molecular cloning and analysis of nucleotide sequence of the
             Bacillus subtilis lysA gene region using B. subtilis phage vectors
             and a multi-copy plasmid, pUB110
JOURNAL   Agric. Biol. Chem. 55 (6), 1615-1626 (1991)
MEDLINE   91345841
REFERENCE   2 (bases 1 to 28206)
AUTHORS   Buchanan,C.E. and Ling,M.L.
TITLE   Isolation and sequence analysis of dacB, which encodes a
             sporulation-specific penicillin-binding protein in Bacillus
             subtilis
JOURNAL   J. Bacteriol. 174 (6), 1717-1725 (1992)
MEDLINE   92193254
REFERENCE   3 (bases 1 to 28206)
AUTHORS   Sorokin,A., Zumstein,E., Azevedo,V., Ehrlich,S.D. and Serror,P.
TITLE   The organization of the Bacillus subtilis 168 chromosome region
             between the spoVA and serA genetic loci, based on sequence data
JOURNAL   Mol. Microbiol. 10 (2), 385-395 (1993)
MEDLINE   95020538
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     source   1..28206
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                     /strain="168"
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                     /db_xref="taxon:1423"
     gene   1..1239
                     /gene="spoVAF"

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              /db_xref="GI:410115"
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              RPDVAANHVLEGHVIIIVDTSPSVIITPTLFHHVQHAEEYRQAPSVGTFLRWVRFFG
              ILASTLFLPIWFLFVLQPDLLPDNMKFIGLNKDTHIPIILQIFLADLGIEFLRMAAIH
              TPTALSTAMGLIAAVLIGQIAIEVGLTSPEVILVVSLAAIGTFTTPSYELSLATNEPS
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gene          1245..2664
              /gene="lysA"
              /note="putative"

-10_signal    1266..1272
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              /note="putative"
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              EAHTHDYITTGQEDSKFGFDLHNQCTERAIEQVLQSEHIQLGVHCHIGSQIFDTAGF
              VLAAEKIFKKLDEWRDSYSFVSKVLNLGGGFGIRYTEDDEPLHATEYVEKIIEAVKEN
              ASRYGFDIPEIWIEPGRSLVGDAGTTLYTVGSQKEVPGVRQYVAVDGGMNDNIRPALY
              QAKYEAAAANRIGEAHDKTVSIAGKCCESGDMLIWDIDLPEVKEGDLLAVFCTGAYGY
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conflict      1610..1616
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              /citation=[1]

conflict      1751..1757
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conflict      2496..2502
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              /citation=[1]

conflict      2504..2510
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terminator    2666..2694
terminator    2666..2694
              /note="ORFX19"

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              VKQVANQELVTTSELGDKIGNENAAALIAKIKEEFAKNGVPDNKADIEKQVDDAASDL
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conflict      3347..3353
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conflict      3413..3419
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conflict      3428..3434
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              /protein_id="AAA67475.1"
              /db_xref="GI:410119"
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conflict      3982..3988
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terminator    4261..4290
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repeat_region 4287..4320
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              /note="putative"

gene          6022..7323
              /gene="sipS"

-10_signal    6045..6051
              /gene="sipS"
              /note="putative"

-35_signal    6683..6688
              /gene="sipS"
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-10_signal    6705..6710
              /gene="sipS"
              /note="putative"

CDS           6740..7294
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              /note="putative"
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              /product="signal peptidase"
              /protein_id="AAA67478.1"
              /db_xref="GI:410122"
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              YPTLHNRERVFVNMTKVIGEFDRGDIVVLNGDDVHYVKRIIGLPGDTVEMKNDQLYI
              NGKKVDEPYLAANKKRAKQDGFDHLTDDFGPVKVPDNKYFVMGDNRRNSMDSRNGLGL
              FTKKQIAGTSKFVFYPFNEMRKTN"

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-10_signal    7410..7416
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CDS           7529..7873
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                IDGLIKVAKVND"
terminator      7872..7911
-35_signal      7937..7942
-10_signal      7960..7965
protein_bind    8126..8137
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                /bound_moiety="MtrB"
CDS             8132..8284
                /note="ORFX5"
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                /transl_table=11
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                DGTAEITRIEEKSNAVYYDLKMDPSLTKTLVLKGSITVDGVSLTIFGLTEDTVTISLI
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CDS             /note="ORFX6"
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CDS             13023..13778
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CDS             13768..14361
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                KTLDELPPLPENAEEDVLQEEADLFFENFNQTFEDIK"
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                    LGNAATPLGIKAMEQMKKLNGNRSEASRSMITFLAVNTSCITLIPTTVIAVRMAYSSK
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conflict            16460..16466
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                    DLIGVVASIIIVTLLFGSA"
terminator          17348..17360
                    /note="for dacB; putative"
-35_signal          17396..17402
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-10_signal          17418..17421
                    /note="putative; ORFX13"
CDS                 17440..18129
                    /note="ORFX13"
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                    /db_xref="GI:410137"
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                    YDTSGLLLLTNDGEFANKLMHPKYEIDKTYVAKVKGIPPKELLRKLERGIRLEEGKTA
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                    TGDARELRLTK"
misc_signal         18150..18170
                    /standard_name="iron box"
misc_signal         18185..18203
                    /note="homology with E. coli Fur-box; putative"
-35_signal          18204..18209
                    /standard_name="Pho-box"
-10_signal          18224..18229
                    /note="homology with E. coli Pho-box; putative"
CDS                 18261..18806
                    /note="ORFX14"
                    /codon_start=1
                    /transl_table=11
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                    /translation="MDNEEKKAFIHSDRHPSRNLRTLVIHLQRCICRQREYIRRSDA
                    PNFVLEDTNGKRIELSDLKGKGVFLNFWGTWCEPCKKEFPYMANQYKHFKSQGVEIVA
                    VNVGESKIAVHNFMKSYGVNFPVVLDTDRQVLDAYDVSPLPTTFLINPEGKVKVVTG
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CDS                 18803..20431
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                    SQTYNKTIDKIWNFFSSVKVGIWLIVITLAASAFGTIFPQEAYLPPGAQADTYYKEQ
                    YGTFGQLYYLLGFHHLYGSWWYLLLIASIGISLVICSLDRVIPLYRALKNQGVRRSPA
                    FLRRQRLFSETVTVLNGESKEKIVTLLKKHHYRIREKEGSILAEKGRFSRWGPYVNHI
                    GLIFLIGAMLRFVPGMYVDETLWVREGETAAIPGTDGKYYLKNNQFSVETYNSKTEK
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                    FAMIWAQLAWTRFWGWDFPKEVWALITFLFYAAYLHRLSRGWHGEKSAWLAVIGFAII
                    MFNLIFVNIVLAGLHSYA"
misc_signal         21645..21660
                    /standard_name="Pho-box"
                    /note="homology with E. coli Pho-box; putative"
misc_signal         complement(21671..21687)
                    /standard_name="Pho-box"
                    /note="homology with E. coli Pho-box; putative"
CDS                 21706..22428
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                    VSLTPKVYELLYFLAKTPDKVDREKLLKEVWQYEFFGDLRTVDTHVKRLREKLNKVS
                    PEAAKKIVTVWGVGYKFEVGAE"
CDS                 22425..24194
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                    LAVKDTTKHTTRYIFLAAGIAIVLTTFAFFLSSRVTYPLRKMREGAQDLAKGKFDTK
                    IPILTQDEIGELATAFNQMGRQLNFHINALNQEKEQLSNILSSMADGVITNIDGTIL
                    VTNPPAERFLQAWYEQNMNIKEGDNLPEAKELFQNAVSTEKEQMIEMTLQGRSWVL
                    LMSPLYAESHVRGAVAVLRDMTERRLDKLREDFIANVSHELRTPISMLQGYSEAIVD
                    DIASSEEDRKEIAQIIYDESLRMGRLVNDLLDLARMESGHTGLHYEKINVNEFLEKII
                    RKFSGVAKEKNIALDHDISLTEEEFMFDEDKMEQVFTNLIDNALRHTSAGGSVSISVH
                    SVKDGLKIDIKDSGSGIPEEDLPFIFERFYKADKARTRGRAGTGLGLAIVNIVEAHN
                    GSITVHSRIDKGTTFSFYIPTKR"
terminator          24231..24263
                    /note="for ORFX18"
misc_signal         24291..24310
                    /standard_name="iron box"
-35_signal          24340..24345
                    /note="homology with E. coli Fur-box; putative"
misc_signal         24340..24356
                    /note="putative; ORFX20-ORFX21"
                    /standard_name="iron box"
-10_signal          24361..24366
                    /note="homology with E. coli Fur-box; putative"
```

```
Initial Score          =      33   Optimized Score        =     279   Significance =  -0.98
Residue Identity       =     47%   Matches                =     344   Mismatches   =    288
Gaps                   =      96   Conservative Substitutions                      =      0
```

```
                                                                 x              10
                                                                 TCAGTTC----TCCTTAGGGGT
                                                                 ||||| |     ||||| ||||
ATAGGGGAAGGGGCCAGTGGACAATGAAGAAAAAGGCGTTTATTCATTCGGACCGGCATCCTTCTCGTT
18250      18260      18270      18280      18290   X 18300      18310
       20         30         40         50         60         70         80
AACATCCCGCCATTCCCGTTGCCACGGAGTCCAGCG-TATAGCTGCCCATGGCGTAGCGGAATGGAGTCGCA
||| ||| |||||| |||| ||||||||||||||| |  | ||||  | ||||||||| ||||||| ||| ||
TTAATCTGCGCACTCGGC-TATACCA---TTTACAACGCTGTATTTGCC--GGCAAAGGAGTATATCCGA
18320      18330      18340       18350      18360       18370      18380
      90        100        110        120        130        140
GGGTAGGGAAGC-CCACAT--GCGC-AG-TCATGCGCCTG----ACCTGTCG-GTTGCG-GCCTTCATA--
|||   || ||| ||||||  | || || | |||| ||||    |||| ||| |||| | |||| ||||
AGGT-CCGACGCCACCGAATTTGTCCTGAGAGATACGAATGGAAACGTATCGAGCCTCAGTGACTTAAAGG
18390      18400      18410      18420      18430       18440      18450
      150        160        170        180        190        200        210
-AAGGGTGATTTTAAG-CCAGCTGGTAGGAATGGATTTA--CGCTCACGAATCGGCGGGGTTGCGCGCCACA
 | ||||| ||||| || |||||||||||| |||||||||  ||||||||||| || |||||||| ||||||
GAAAGGTGTTTTTTTGAATTCTGGGGTACATGGTGTGAACCGTGCAAAAAAGAGTTTCCTTATATCGCA-A
18460      18470      18480      18490      18500      18510      18520
      220        230        240        250        260        270
GCCACT-----CGGGTTCATTCACA--CGTTCA-ATACCAGCCGCAGGGTGGGACCGTC---GTTCAGCG
|||||      ||||||||||| |||  || |||  |||||||| | ||||||||||||||    |||||||
ACCAATATAAGCATTTTAAAGCCAAGTGTTGAAATTGTCGCTGAAATGTGGGGAGTCAAAGAT-AGCA
18530      18540      18550      18560      18570      18580      18590
      280        290        300        310        320        330        340
TTACGCCGTTGCGCAGCTTTGCCAGCGACGCGCTCGTCCGGCTCGCCCTTCAACCTGCACATAGTAAATT--TT
||||||||||| |||||||||||||| ||| || ||||| || || ||||| |||||| ||||| |||||  ||
GTACATAATT-TTATGAAATCCTACGGAGTCAATTTCCCGGTTG--TTCTGGATACAGATCGCCAAGTGCTT
18600      18610      18620      18630      18640      18650      18660
      350        360        370        380        390        400        410
--T-CCGGT-ACGTTGCCCGGCTGAGTAAGCCTGGCGTGGAGCCACGCCGTCATTGGTAAGGACCAGCAGCC
  | |||||  ||| |||||||||||| ||||||||| ||||| |||||||||| ||||||||| |||||||
GATCCTATGACGTATCTCCGCGTTCCGACAACCT--TTTTGATCAATCCGAA--GGAAAAGTTGTCAAGGT
18670      18680      18690      18700      18710      18720      18730
      420        430        440        450        460        470        480
CCTCGCTGTCGCGAT-CCAGACGTCCCGCTGCGTAGACTCCCTGTACGGGGATAAAGTCCTTCAGCGTGCTG
|| ||| | ||||| | |||||| || | || ||| |  | | |||| ||||| ||||| ||||||||||||
CG--TGCGG---AAGAGCTCTTCAGGAAACTCAACCTCCGC----TCGCTGCTATGACGAGATGACGGAAGCG
18740      18750      18760      18770      18780      18790      18800
      490        500        510        520        530        540
CGCCCGG--CCTCGTC---GGTAAACTGCGG-CA-ATACATCGTAGGGTTTATTGAACAGTATGACCCGCGT
|| ||||  ||||| ||   |||||||||||  || | |||| || ||| |||||||||||||||||||||||
CGGGATGAAGCAAGTCAAATGTGAA-TGCGGACATATAAACC----CGGT--CGGAACCGTTTTATGCGAAT
18810      18820      18830      18840      18850      18860
      550        560        570        580        590        600        610        620
TGCCTGGGGTTCTGGCGTTCTTCGGTGGCGTTCGCTGAGCTGAATCGGCTCGAATCGCTCA-ACCCGTGTTCTTCTAAAAG
|| |||||| ||||||| | ||| | || || |||||| || |  | |||  || |||  |  |||||||| ||||||||||
CG--TGCGG---AAGAGCTCTTCAGGAAACTCAACCTCCGC----TCGCTGCTATGACGAGATGACGGAAGCG
18870      18880      18890      18900      18910      18920
      630        640        650        660
-AAG-TTTTCCTCATGGTATTTTCAGGCG-TTATC---AATTGCCGCATT--ATAGC
 |||   |||||||| ||| |||||||||  |||||    |||||| |||    ||||
CAAGACGTTCGCAAACCTATAACAAAACCATCATCGACAAAAATTGGAATTTCCGGTTAGGTGG
18930      18940      18950      18960      18970      18980   X 18990

GAATATGGCTTATCGTCATAACCCTTGCCGCATCAG
19000      19010      19020      19030
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CDS
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        /db_xref="GI:410143"
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        YHTFEGRSSEKTWLLSIARHVAIDWFRKQQTIRQRILGTFDWDTQDVRDQQLLPDELA
        VQHENVREISCALDQCTIDQRAVIILRFIQGYSIQETAKALRFSESKVKTTQHRGLKV
        LRKHMELLREELMDDEVRMERRTDKGVVKSTSGS"
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CDS
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24918..26024
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        /codon_start=1
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        /protein_id="AAA67500.1"
        /db_xref="GI:410144"
        /translation="MMKSEWNEEQIKELLSQLPAVKDHRSPQDIYKRLTMAKRKNKPA
        VRWIGPACAAIAVYIAFIISPHFFDQAPQQKEASQENAVTKTETEDSPKAASSLDQ
        TSFVVPEKEQDNIVTVAVADADTSAIIPVSIOKTNADQTIQDMLFESSELGILDHAIT
        IPFFIDEVEIKERPKQKELSIRVHQPATAFSIKDDTLLKKLLKESLKWSPYEKVKFLS
        DQNETGVRIGSYGTFTEISIPKQSKRSYYLLYQNKQGQDFLVPSNHSFDTVKEAIKEME
        SSSQEDTTPLIQAGAVQSVTKKOKHLYMRFSKESEVDDSIAGILMIEGLLLTAKEFGF
        TEVIFTETRTKKIGKYDISDAIPVPAAPNPISLN"
```

terminator
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26019..26053
        /note="for ORFX20-ORFX21; putative"
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gene
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26073..26903
        /gene="aroC"
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-35_signal
```
26073..26078
        /gene="aroC"
```

-10_signal
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26096..26101
        /gene="aroC"
        /note="putative"
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protein_bind
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26130..26139
        /gene="aroC"
        /note="putative"
        /bound_moiety="MtrB"
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CDS
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26909..26903
        /gene="aroC"
        /note="for aroC"
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        /transl_table=11
        /product="dehydroquinate dehydratase"
        /protein_id="AAA67501.1"
        /db_xref="GI:410145"
        /translation="MNVLIIKGVSIGEGMPKIIIPLMGKTEKQILNERAVKLLNPDI
        VEWRVDVFEKANDREAVTKLISKLRKSLEDKLFLFTFRTHKEGGSMEMDESSYIALLE
        SAIQTKDIDLIDIELFSGDANVKALVSLAEENVYVVMSNHDFEKTPVKDEIISLRK
        MQDLGAHIPKMAVMPNDTGDLLTLLDATYTMKTIYADRPIITMSMAATGLISRLSGEV
        FGSACTFGAGEEASAPGQIPVSELRSVLDILHKNTRG"
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terminator
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26909..26944
        /gene="serA"
        /note="for aroC"
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gene
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complement(26946..28206)
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CDS
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complement(26946..>28206)
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        /transl_table=11
        /product="phosphoglycerate dehydrogenase"
        /protein_id="AAA67502.1"
        /db_xref="GI:410116"
        /translation="ISSLMRHIPQANISVKSREWNRTAYVGSELYGKTLGIVGLGRIG
        SEIAQRRGAFGMTVHVFDPFLTEERAKKICVNSRTFEEVLESADIITVHTPLTKETKG
        LLNKETIAKITKKGVRLINCARGGIIDEAALLEALENGHVAGAALDVFEVEPPVDNKLV
        DHPLVIATPHLGASTKEAQLNVAAQVSEEVLQFAKGLPVMSAINLPAMTKDEFAKIKP
        YHQIAGKIGSLVSQCMKEPVQDVAIQYEGTIAKLETSFITKALLSGFLKPRVDSTVNE
        VNAGGVAKERGISFSEKISSSESGSGYDNCISVKVTGDRSTFTVTATYIPHFGERIVEIN
        GFNIDFYPTGHLVYIQHQDTTGVIGRVGRILGDNDINIATMQVGRKEKGGEAIMMLSF
        DRHLEDKIVKELTNVPDIVSVKLIDLP"
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BASE COUNT   8529 a   5565 c   6530 g   7582 t
ORIGIN

L09228   Length: 28206   September 24, 2001 09:27   Type: N   Check: 8816   ..